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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 28
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-242-074-28

Query Match      84.6%; Score 899; DB 12; Length 175;
Best Local Similarity 100.0%; Pred. No. 2.1e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 MEKIPVSALLLVALLSYTLARDTTVKPGAKDVKDSRPKLPQTLRSRGWDQLIWTQYEE 91
Db 1 MEKIPVSALLLVALLSYTLARDTTVKPGAKDVKDSRPKLPQTLRSRGWDQLIWTQYEE 60

QY 92 ALYKSTNSKPLMIHLLDECPHSQALKKVFPAENKEIOKLAEOQVLLNLVYETTDKHLSP 151
Db 61 ALYKSTNSKPLMIHLLDECPHSQALKKVFPAENKEIOKLAEOQVLLNLVYETTDKHLSP 120

QY 152 DGQVPRIMFVDPSTVRADITGRYSNRLYAYEPADTALLDDNMKKALKLKTTEL 206
Db 121 DGQVPRIMFVDPSTVRADITGRYSNRLYAYEPADTALLDDNMKKALKLKTTEL 175

RESULT 5
US-10-242-505-28
; Sequence 28, Application US/10242505
; Publication No. US20030138898A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C25
; CURRENT APPLICATION NUMBER: US/10/242,505
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/079689

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; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 28
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-242-505-28

Query Match      84.6%; Score 899; DB 12; Length 175;
Best Local Similarity 100.0%; Pred. No. 2.1e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 MEKIPVSALLLVALLSYTLARDTTVKPGAKDVKDSRPKLPQTLRSRGWDQLIWTQYEE 91
Db 1 MEKIPVSALLLVALLSYTLARDTTVKPGAKDVKDSRPKLPQTLRSRGWDQLIWTQYEE 60

QY 92 ALYKSTNSKPLMIHLLDECPHSQALKKVFPAENKEIOKLAEOQVLLNLVYETTDKHLSP 151
Db 61 ALYKSTNSKPLMIHLLDECPHSQALKKVFPAENKEIOKLAEOQVLLNLVYETTDKHLSP 120

QY 152 DGQVPRIMFVDPSTVRADITGRYSNRLYAYEPADTALLDDNMKKALKLKTTEL 206
Db 121 DGQVPRIMFVDPSTVRADITGRYSNRLYAYEPADTALLDDNMKKALKLKTTEL 175

RESULT 6
US-10-242-574-28
; Sequence 28, Application US/10242574
; Publication No. US20030138899A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C20
; CURRENT APPLICATION NUMBER: US/10/242,574
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801

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; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 28
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-242-574-28

Query Match      84.6%; Score 899; DB 12; Length 175;
Best Local Similarity 100.0%; Pred. No. 2.1e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 MEKIPVSFALLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDLIWTQYEE 91
Db 1 MEKIPVSFALLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDLIWTQYEE 60
QY 92 ALYKSTSNKPLMIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP 151
Db 61 ALYKSTSNKPLMIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP 120
QY 152 DGQYVPRIMFVDPSTLRADITGRYSNRLYAYEPADTALLDNMKKALKLLKTEL 206
Db 121 DGQYVPRIMFVDPSTLRADITGRYSNRLYAYEPADTALLDNMKKALKLLKTEL 175

RESULT 7
US-10-243-261-28
; Sequence 28, Application US/10243261
; Publication No. US20030138900A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C56
; CURRENT APPLICATION NUMBER: US/10/243,261
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 28
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-243-261-28

Query Match      84.6%; Score 899; DB 12; Length 175;
Best Local Similarity 100.0%; Pred. No. 2.1e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 MEKIPVSFALLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDLIWTQYEE 91
Db 1 MEKIPVSFALLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDLIWTQYEE 60
QY 92 ALYKSTSNKPLMIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP 151
Db 61 ALYKSTSNKPLMIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP 120
QY 152 DGQYVPRIMFVDPSTLRADITGRYSNRLYAYEPADTALLDNMKKALKLLKTEL 206
Db 121 DGQYVPRIMFVDPSTLRADITGRYSNRLYAYEPADTALLDNMKKALKLLKTEL 175

RESULT 8
US-10-243-282-28
; Sequence 28, Application US/10243282
; Publication No. US20030138901A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C50
; CURRENT APPLICATION NUMBER: US/10/243,282
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 28
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-243-282-28
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; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 28
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-242-574-28

Query Match      84.6%; Score 899; DB 12; Length 175;
Best Local Similarity 100.0%; Pred. No. 2.1e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 MEKIPVSFALLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDLIWTQYEE 91
Db 1 MEKIPVSFALLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDLIWTQYEE 60
QY 92 ALYKSTSNKPLMIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP 151
Db 61 ALYKSTSNKPLMIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP 120
QY 152 DGQYVPRIMFVDPSTLRADITGRYSNRLYAYEPADTALLDNMKKALKLLKTEL 206
Db 121 DGQYVPRIMFVDPSTLRADITGRYSNRLYAYEPADTALLDNMKKALKLLKTEL 175

RESULT 7
US-10-243-261-28
; Sequence 28, Application US/10243261
; Publication No. US20030138900A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C56
; CURRENT APPLICATION NUMBER: US/10/243,261
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 28
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-243-261-28
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Query Match 84.6%; Score 899; DB 12; Length 175;  
Best Local Similarity 100.0%; Pred. No. 2.1e-92;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 MEKIPVSAFLLLVSLYTLARDTTVKPGAKKDTKDSRPKLPOTLSRGWGDLWTQTYEE 91  
DB 1 MEKIPVSAFLLLVSLYTLARDTTVKPGAKKDTKDSRPKLPOTLSRGWGDLWTQTYEE 60

QY 92 ALYKSKTSNKPMLIIHHLDECPHSQALKVFAENKEIQKLAEOQVLLNLVYETTDKHLSP 151  
DB 61 ALYKSKTSNKPMLIIHHLDECPHSQALKVFAENKEIQKLAEOQVLLNLVYETTDKHLSP 120

QY 152 DQGVPRIMFVDPSSLTVRADITGRYSNRLYAYEPADTALLDDNMKALKLKTTEL 206  
DB 121 DQGVPRIMFVDPSSLTVRADITGRYSNRLYAYEPADTALLDDNMKALKLKTTEL 175

RESULT 9  
US-10-243-402-28  
; Sequence 28, Application US/10243402  
; Publication No. US20030138902A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3630R1C39  
; CURRENT APPLICATION NUMBER: US/10/243,402  
; CURRENT FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; PRIOR FILING DATE: 1998-06-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO: 28  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-243-402-28

Query Match 84.6%; Score 899; DB 12; Length 175;  
Best Local Similarity 100.0%; Pred. No. 2.1e-92;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 MEKIPVSAFLLLVSLYTLARDTTVKPGAKKDTKDSRPKLPOTLSRGWGDLWTQTYEE 91  
DB 1 MEKIPVSAFLLLVSLYTLARDTTVKPGAKKDTKDSRPKLPOTLSRGWGDLWTQTYEE 60

DB 1 MEKIPVSAFLLLVSLYTLARDTTVKPGAKKDTKDSRPKLPOTLSRGWGDLWTQTYEE 60

QY 92 ALYKSKTSNKPMLIIHHLDECPHSQALKVFAENKEIQKLAEOQVLLNLVYETTDKHLSP 151  
DB 61 ALYKSKTSNKPMLIIHHLDECPHSQALKVFAENKEIQKLAEOQVLLNLVYETTDKHLSP 120

QY 152 DQGVPRIMFVDPSSLTVRADITGRYSNRLYAYEPADTALLDDNMKALKLKTTEL 206  
DB 121 DQGVPRIMFVDPSSLTVRADITGRYSNRLYAYEPADTALLDDNMKALKLKTTEL 175

RESULT 10  
US-10-243-431-28  
; Sequence 28, Application US/10243431  
; Publication No. US20030138903A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3630R1C37  
; CURRENT APPLICATION NUMBER: US/10/243,431  
; CURRENT FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; PRIOR FILING DATE: 1998-06-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO: 28  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-243-431-28

Query Match 84.6%; Score 899; DB 12; Length 175;  
Best Local Similarity 100.0%; Pred. No. 2.1e-92;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 MEKIPVSAFLLLVSLYTLARDTTVKPGAKKDTKDSRPKLPOTLSRGWGDLWTQTYEE 91  
DB 1 MEKIPVSAFLLLVSLYTLARDTTVKPGAKKDTKDSRPKLPOTLSRGWGDLWTQTYEE 60

QY 92 ALYKSKTSNKPMLIIHHLDECPHSQALKVFAENKEIQKLAEOQVLLNLVYETTDKHLSP 151  
DB 61 ALYKSKTSNKPMLIIHHLDECPHSQALKVFAENKEIQKLAEOQVLLNLVYETTDKHLSP 120

QY 152 DQYVPRIMFVDPSTVTRADITGRYSNRLYAYEPADTALLDNNMKKALKLKTTEL 206  
Db 121 DQYVPRIMFVDPSTVTRADITGRYSNRLYAYEPADTALLDNNMKKALKLKTTEL 175

## RESULT 11

US-10-245-164-28  
; Sequence 28, Application US/10245164  
; Publication No. US20030138904A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3630R1C76  
; CURRENT APPLICATION NUMBER: US/10/245,164  
; PRIOR FILING DATE: 2002-09-16  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR FILING DATE: 1998-06-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 28  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: Homo Sapien

US-10-245-164-28  
Query Match 84.6%; Score 899; DB 12; Length 175;  
Best Local Similarity 100.0%; Pred. No. 2.1e-92;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 MEKIPVSFLLLVSLYTLARDTTVPKAKKDTKDSRPKLPQTLRSRGWDQLIWTQYEE 91  
Db 1 MEKIPVSFLLLVSLYTLARDTTVPKAKKDTKDSRPKLPQTLRSRGWDQLIWTQYEE 60  
QY 92 ALYKSTSNKPLMIHHLDECPHSQALKKVFANKEIQKLAEOFVLLNLVYETTDKHLSP 151  
Db 61 ALYKSTSNKPLMIHHLDECPHSQALKKVFANKEIQKLAEOFVLLNLVYETTDKHLSP 120  
QY 152 DQYVPRIMFVDPSTVTRADITGRYSNRLYAYEPADTALLDNNMKKALKLKTTEL 206  
Db 121 DQYVPRIMFVDPSTVTRADITGRYSNRLYAYEPADTALLDNNMKKALKLKTTEL 175

## RESULT 12

US-09-903-190-106  
; Sequence 106, Application US/09903190  
; Publication No. US20030162176A1  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Bougueleret, Lydie  
; TITLE OF INVENTION: Complementary DNAs  
; FILE REFERENCE: GENSET.021A  
; CURRENT APPLICATION NUMBER: US/09/903,190  
; CURRENT FILING DATE: 2001-07-11  
; PRIOR APPLICATION NUMBER: US/09/247,155A  
; PRIOR FILING DATE: 1999-02-09  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/074,121  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/081,563  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-13  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/096,116  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-10  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/099,273  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-04  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: Patent.pm  
; SEQ ID NO 106  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -20...-1  
US-09-903-190-106

Query Match 84.6%; Score 899; DB 12; Length 175;  
Best Local Similarity 100.0%; Pred. No. 2.1e-92;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 MEKIPVSFLLLVSLYTLARDTTVPKAKKDTKDSRPKLPQTLRSRGWDQLIWTQYEE 91  
Db 1 MEKIPVSFLLLVSLYTLARDTTVPKAKKDTKDSRPKLPQTLRSRGWDQLIWTQYEE 60  
QY 92 ALYKSTSNKPLMIHHLDECPHSQALKKVFANKEIQKLAEOFVLLNLVYETTDKHLSP 151  
Db 61 ALYKSTSNKPLMIHHLDECPHSQALKKVFANKEIQKLAEOFVLLNLVYETTDKHLSP 120  
QY 152 DQYVPRIMFVDPSTVTRADITGRYSNRLYAYEPADTALLDNNMKKALKLKTTEL 206  
Db 121 DQYVPRIMFVDPSTVTRADITGRYSNRLYAYEPADTALLDNNMKKALKLKTTEL 175

## RESULT 13

US-10-244-972-28  
; Sequence 28, Application US/10244972  
; Publication No. US20030170809A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3630R1C75  
; CURRENT APPLICATION NUMBER: US/10/244, 972  
; CURRENT FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: 10/197942

US-10-244-972-28  
Query Match 84.6%; Score 899; DB 12; Length 175;  
Best Local Similarity 100.0%; Pred. No. 2.1e-92;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 MEKIPVSFLLLVSLYTLARDTTVPKAKKDTKDSRPKLPQTLRSRGWDQLIWTQYEE 91  
Db 1 MEKIPVSFLLLVSLYTLARDTTVPKAKKDTKDSRPKLPQTLRSRGWDQLIWTQYEE 60  
QY 92 ALYKSTSNKPLMIHHLDECPHSQALKKVFANKEIQKLAEOFVLLNLVYETTDKHLSP 151  
Db 61 ALYKSTSNKPLMIHHLDECPHSQALKKVFANKEIQKLAEOFVLLNLVYETTDKHLSP 120  
QY 152 DQYVPRIMFVDPSTVTRADITGRYSNRLYAYEPADTALLDNNMKKALKLKTTEL 206  
Db 121 DQYVPRIMFVDPSTVTRADITGRYSNRLYAYEPADTALLDNNMKKALKLKTTEL 175

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; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
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; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091358
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
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; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 60/115554
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; PRIOR FILING DATE: 1999-04-27
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; PRIOR APPLICATION NUMBER: 60/149327
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; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/151700
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/151734
; PRIOR FILING DATE: 1999-08-31

Query Match      84.6%; Score 899; DB 12; Length 175;
Best Local Similarity 100.0%; Pred. No. 2.1e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 MEKIPVSALLLVSLYTLARDTTVKCGAKDXTKDSRPKLPQTLSRGNGDQLIWTQYEE 91
Db 1 MEKIPVSALLLVSLYTLARDTTVKCGAKDXTKDSRPKLPQTLSRGNGDQLIWTQYEE 60

Qy 92 ALYKSTNSKPLMIHHLDECPHSQALKKVPFAENKGIQKLAEQFVLLNLVYTTDKHLSP 151
Db 61 ALYKSTNSKPLMIHHLDECPHSQALKKVPFAENKGIQKLAEQFVLLNLVYTTDKHLSP 120

Qy 152 DGQVPRIMFVDPSTVRADITGRYSNRLYAYEPADTALLLDNNKKALKLKLTEL 206
Db 121 DGQVPRIMFVDPSTVRADITGRYSNRLYAYEPADTALLLDNNKKALKLKLTEL 175

RESULT 14
US-10-197-942-28
; Sequence 28, Application US/10197942
; Publication No. US20030175882A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C1(US)
; CURRENT APPLICATION NUMBER: US/10/197,942
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
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PRIOR APPLICATION NUMBER: 60/162506  
PRIOR FILING DATE: 1999-10-29  
PRIOR APPLICATION NUMBER: 60/170262  
PRIOR FILING DATE: 1999-12-09  
PRIOR APPLICATION NUMBER: 60/177118  
PRIOR FILING DATE: 2000-01-20  
PRIOR APPLICATION NUMBER: 60/179851  
PRIOR FILING DATE: 2000-02-02  
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PRIOR FILING DATE: 2000-02-08  
PRIOR APPLICATION NUMBER: 60/187202  
PRIOR FILING DATE: 2000-03-03  
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PRIOR FILING DATE: 2000-04-18  
PRIOR APPLICATION NUMBER: 60/199614  
PRIOR FILING DATE: 2000-04-25  
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PRIOR FILING DATE: 2000-05-23  
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PRIOR FILING DATE: 1998-11-19  
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PRIOR FILING DATE: 1999-03-12  
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PRIOR FILING DATE: 1999-08-25  
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PRIOR FILING DATE: 1999-08-25  
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PRIOR FILING DATE: 1999-11-10  
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PRIOR APPLICATION NUMBER: 09/802706

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PRIOR APPLICATION NUMBER: 09/872035  
PRIOR FILING DATE: 2001-06-01  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
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PRIOR APPLICATION NUMBER: 09/931836  
PRIOR FILING DATE: 2001-08-16  
PRIOR APPLICATION NUMBER: 09/941992  
PRIOR FILING DATE: 2001-08-28  
PRIOR APPLICATION NUMBER: 09/946374  
PRIOR FILING DATE: 2001-09-04  
PRIOR APPLICATION NUMBER: 10/001054  
PRIOR FILING DATE: 2001-11-30  
PRIOR APPLICATION NUMBER: 10/052586  
PRIOR FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: 10/081056  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: 10/119480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: PCT/US98/18824  
PRIOR FILING DATE: 1998-09-10

Query Match 84.6%; Score 899; DB 12; Length 175;  
Best Local Similarity 100.0%; Pred. No. 2.1e-92;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 MEKIPVSAFLLVLSYTLARDTTVKPGAKKDTKOSRKLPTLSRGWGDQLIWTQYEE 91  
DB 1 MEKIPVSAFLLVLSYTLARDTTVKPGAKKDTKOSRKLPTLSRGWGDQLIWTQYEE 60

QY 92 ALYKSKTSNKPLMIHHLDECPSHQSALKKVFAENKEIQKLAQFVLLNLVYETTDKHLSP 151  
DB 61 ALYKSKTSNKPLMIHHLDECPSHQSALKKVFAENKEIQKLAQFVLLNLVYETTDKHLSP 120

QY 152 DGQYVPRIMFVDPSTLVRADITGRYSNRLYAYEPADTALLDNMKKALKLLKTEL 206  
DB 121 DGQYVPRIMFVDPSTLVRADITGRYSNRLYAYEPADTALLDNMKKALKLLKTEL 175

RESULT 15  
US-10-238-196-28  
Sequence 28, Application US/10238196  
Publication No. US20030186372A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin  
APPLICANT: Eaton, Dan  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe  
APPLICANT: Watanabe, Colin  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
APPLICANT: Fong, Sherman  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3630R1C8  
CURRENT APPLICATION NUMBER: US/10/238,196  
CURRENT FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 10/197942  
PRIOR FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 60/059114  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/063046  
PRIOR FILING DATE: 1997-10-24

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; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 28
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-238-196-28

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Query Match      84.6%; Score 899; DB 12; Length 175;
Best Local Similarity 100.0%; Pred. No. 2.le-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 MEKIPVSFLLLVLSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDOLIWTQYEE 91
Db 1 MEKIPVSFLLLVLSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDOLIWTQYEE 60

Qy 92 ALYKSKTSNKPLMIHHLDCEPHSQALKKVFPAENKEIQKLAEQFVLLNLVYETDDKHLSP 151
Db 61 ALYKSKTSNKPLMIHHLDCEPHSQALKKVFPAENKEIQKLAEQFVLLNLVYETDDKHLSP 120

Qy 152 DGQYVPRIMFVDPSTLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLKTTEL 206
Db 121 DGQYVPRIMFVDPSTLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLKTTEL 175

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Job time : 32 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 26, 2003, 15:53:44 ; Search time 21 Seconds  
(without alignments)  
415.049 Million cell updates/sec

Title: US-09-674-266A-181  
Perfect score: 1063  
Sequence: 1 RLSCAGTSGSGPHPSRLT.....DTALLDNMKALKLKTLEL 206

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Issued Patents AA.\*
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  - 2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pap.\*
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  - 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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4	605	56.9	131	4	US-09-247-155-174
5	555	52.2	166	3	US-08-916-576B-6
6	448	42.1	183	3	US-08-916-576B-7
7	222	20.9	172	3	US-08-916-576B-4
8	88.5	8.3	118	4	US-09-198-452A-1234
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10	81.5	7.7	901	3	US-09-258-643-5
11	81.5	7.7	968	3	US-08-560-005-7
12	81.5	7.7	968	3	US-09-418-540-7
13	81.5	7.7	968	4	US-09-969-528-7
14	79	7.4	166	4	US-09-198-452A-998
15	78	7.3	129	4	US-09-534-638-5
16	78	7.3	453	3	US-09-013-881-5
17	78	7.3	453	4	US-09-612-473-5
18	78	7.3	1160	5	PCT-US92-05401-4
19	77	7.2	652	2	US-08-313-185-53
20	77	7.2	652	2	US-08-459-499-17
21	77	7.2	652	3	US-09-082-614A-53
22	77	7.2	1049	4	US-09-107-532A-5966
23	74.5	7.0	2321	4	US-09-230-652-2
24	74	7.0	264	3	US-09-053-197A-8
25	74	7.0	264	4	US-09-085-761A-8
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27	73	6.9	1067	4	US-09-107-532A-5148

28	71.5	6.7	352	3	US-08-921-887-52	Sequence 52, Appl
29	71.5	6.7	382	4	US-09-134-001C-3765	Sequence 3765, Ap
30	71.5	6.7	508	4	US-09-252-991A-32765	Sequence 32765, A
31	71.5	6.7	588	4	US-09-328-352-7994	Sequence 7994, Ap
32	71.5	6.7	698	4	US-09-107-532A-5685	Sequence 5685, Ap
33	71	6.7	529	3	US-08-821-984-6	Sequence 6, Appli
34	71	6.7	529	3	US-08-821-984-8	Sequence 8, Appli
35	71	6.7	529	3	US-09-329-749-6	Sequence 6, Appli
36	71	6.7	529	3	US-09-329-749-8	Sequence 8, Appli
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40	70.5	6.6	481	1	US-08-311-611A-98	Sequence 98, Appl
41	70.5	6.6	481	1	US-08-372-783-98	Sequence 98, Appl
42	70.5	6.6	481	1	US-08-372-105-98	Sequence 98, Appl
43	70.5	6.6	481	1	US-08-306-473A-98	Sequence 98, Appl
44	70.5	6.6	481	1	US-08-261-660A-4	Sequence 4, Appli
45	70.5	6.6	481	1	US-08-209-762-98	Sequence 98, Appl

ALIGNMENTS

RESULT 1  
US-08-916-576B-2  
; Sequence 2, Application US/08916576B  
; Patent No. 6171816  
; GENERAL INFORMATION:  
; APPLICANT: YU, GUO-LIANG  
; APPLICANT: DILLON, PATRICK J.  
; APPLICANT: EBNER, REINHARD  
; APPLICANT: ENDRESS, GREGORY A.  
; TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 NEW YORK AVENUE, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: US  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/916,576B  
; FILING DATE:  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/024,347  
; FILING DATE: 23-AUG-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0500001  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 175 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-916-576B-2

Query Match 84.6%; Score 899; DB 3; Length 175;  
Best Local Similarity 100.0%; Pred. No. 1.6e-95;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 MEKIPVSAPLLVALSYTLARDTTVRPGAKKDTKDSRKLPTQLSRGWGDLIWTQTYEE 91

Db 1 MEKIPVSALLVSLVLTARDITVPGAKKDTKDSRPKLPQTLSRGWGDLWTQTYEE 60  
QY 92 ALYKSTSNKPLMIHHLDECPHSQALKVFAENKEIQKLAQFVLLNLVYETTDKHLSP 151  
Db 61 ALYKSTSNKPLMIHHLDECPHSQALKVFAENKEIQKLAQFVLLNLVYETTDKHLSP 120  
QY 152 DGQYVPRIMFVPSLTVRADITGRYSNRLYAYEPADTALLDNKKALKLLKTEL 206  
Db 121 DGQYVPRIMFVPSLTVRADITGRYSNRLYAYEPADTALLDNKKALKLLKTEL 175

RESULT 2

US-09-247-155-106  
; Sequence 106, Application US/09247155A  
; Patent No. 6312922  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Bougueleret, Lydie  
; FILE REFERENCE: GENSET.021A  
; CURRENT APPLICATION NUMBER: US/09/247,155A  
; CURRENT FILING DATE: 1999-02-09  
; EARLIER APPLICATION NUMBER: 60/074,121  
; EARLIER FILING DATE: 1998-02-09  
; EARLIER APPLICATION NUMBER: 60/081,563  
; EARLIER FILING DATE: 1998-04-13  
; EARLIER APPLICATION NUMBER: 60/096,116  
; EARLIER FILING DATE: 1998-08-10  
; EARLIER APPLICATION NUMBER: 60/099,273  
; EARLIER FILING DATE: 1998-10-04  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: Patent.pm  
; SEQ ID NO 106  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -20..-1  
US-09-247-155-106

Query Match 84.6%; Score 899; DB 4; Length 175;  
Best Local Similarity 100.0%; Pred. No. 1.6e-95;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 MEKIPVSALLVSLVLTARDITVPGAKKDTKDSRPKLPQTLSRGWGDLWTQTYEE 91  
Db 1 MEKIPVSALLVSLVLTARDITVPGAKKDTKDSRPKLPQTLSRGWGDLWTQTYEE 60  
QY 92 ALYKSTSNKPLMIHHLDECPHSQALKVFAENKEIQKLAQFVLLNLVYETTDKHLSP 151  
Db 61 ALYKSTSNKPLMIHHLDECPHSQALKVFAENKEIQKLAQFVLLNLVYETTDKHLSP 120  
QY 152 DGQYVPRIMFVPSLTVRADITGRYSNRLYAYEPADTALLDNKKALKLLKTEL 206  
Db 121 DGQYVPRIMFVPSLTVRADITGRYSNRLYAYEPADTALLDNKKALKLLKTEL 175

RESULT 3

US-08-916-576B-8  
; Sequence 8, Application US/08916576B  
; Patent No. 6171816  
; GENERAL INFORMATION:  
; APPLICANT: YU GUO-LIANG  
; APPLICANT: DILLON, PATRICK J.  
; APPLICANT: EBNER, REINHARD  
; APPLICANT: ENDRESS, GREGORY A.  
; TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.

; STREET: 1100 NEW YORK AVENUE, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: US  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/916,576B  
; FILING DATE:  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/024,347  
; FILING DATE: 23-AUG-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0500001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 170 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-916-576B-8

Query Match 57.3%; Score 609.5; DB 3; Length 170;  
Best Local Similarity 71.3%; Pred. No. 3.2e-62;  
Matches 122; Conservative 14; Mismatches 26; Indels 9; Gaps 2;  
QY 37 VSAFLLVSLVLTARDITVPGAKKDTKDSRP-KLPQTLSRGWGDLWTQTYEEALYK 95  
Db 7 LGACLLVSLVSLA-----XXXKGKDXRPKPGQTLSRGWGDXIXWVQTYEGLAK 58  
QY 96 SKTSNKLPMIHHLDCEPHSQALKVFAENKEIQKLAQFVLLNLVYETTDKHLSPDGQY 155  
Db 59 AXSNKPLMVIHLEDCPYSQLKVVFAENXIQELAQNFMVNLVHETTDENSLSPDGQY 118  
QY 156 VPRIMFVPSLTVRADITGRYSNRLYAYEPADTALLDNKKALKLLKTEL 206  
Db 119 VPRIMFVPSLTVRADITGRYSNRLYAYEPDXDPLLIKNKKALKLLKTEL 169

RESULT 4

US-09-247-155-174  
; Sequence 174, Application US/09247155A  
; Patent No. 6312922  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Bougueleret, Lydie  
; TITLE OF INVENTION: Complementary DNAs  
; FILE REFERENCE: GENSET.021A  
; CURRENT APPLICATION NUMBER: US/09/247,155A  
; CURRENT FILING DATE: 1999-02-09  
; EARLIER APPLICATION NUMBER: 60/074,121  
; EARLIER FILING DATE: 1998-02-09  
; EARLIER APPLICATION NUMBER: 60/081,563  
; EARLIER FILING DATE: 1998-04-13  
; EARLIER APPLICATION NUMBER: 60/096,116  
; EARLIER FILING DATE: 1998-08-10  
; EARLIER APPLICATION NUMBER: 60/099,273  
; EARLIER FILING DATE: 1998-10-04  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: Patent.pm  
; SEQ ID NO 174

LENGTH: 131

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SIGNAL

LOCATION: -20...-1

FEATURE: UNSURE

NAME/KEY: UNSURE

LOCATION: 40,41,43,60,70,76,82,86,105,107

OTHER INFORMATION: Xaa = any one of the twenty amino acids

US-09-247-155-174

Query Match

Best Local Similarity 56.9%; Score 605; DB 4; Length 131;

Mismatches 9; Indels 0; Gaps 0;

Matches 117; Conservative 9; Indels 0; Gaps 0;

Qy 32 MEKIPVSAPLILVALSYTLARDTTVKCAKDTKDSRPKLPQTLSRGWDQDLIWTQYEE 91

Db 1 MEKIPVSAPLILVALSYTLARDTTVKCAKDTKDSRPKLPQTLSRGWDQDLIWTQYEX 60

Qy 92 ALYKSKTSNKPLMIHHLDECPSQALKKVFAPENKEIOKLAEQFVLLNLVYETTDKHLSP 151

Db 61 XLKSKTSNKPLMIHHLDECPSQALKKVFAPENKXIOKLAEQFVLLNLVYETTDKHLSP 120

Qy 152 DGQXP 157

Db 121 DGQXP 126

RESULT 5

US-08-916-576B-6

; Sequence 6, Application US/08916576B

; Patent No. 6171816

; GENERAL INFORMATION:

; APPLICANT: YU, GUO-LIANG

; APPLICANT: DILLON, PATRICK J.

; APPLICANT: EBNER, REINHARD

; APPLICANT: ENDRESS, GREGORY A.

; TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS

; NUMBER OF SEQUENCES: 45

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.

; STREET: 1100 NEW YORK AVENUE, SUITE 600

; CITY: WASHINGTON

; STATE: DC

; COUNTRY: US

; ZIP: 20005-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/916,576B

; FILING DATE:

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/024,347

; FILING DATE: 23-AUG-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: STEFFE, ERIC K.

; REGISTRATION NUMBER: 36,688

; REFERENCE/DOCKET NUMBER: 1488.0500001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 166 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-916-576B-6

Query Match

Best Local Similarity 52.2%; Score 555; DB 3; Length 166;

Mismatches 28; Conservative 19; Indels 12; Gaps 4;

Matches 108; Conservative 28; Mismatches 19; Indels 12; Gaps 4;

Qy 41 LLLVALSYTLARDTTVKGAKKDTKDSRPKLPQTLSRGWDQDLIWTQYEEALYKSKTSN 100

Db 11 LLLVTVSSNLA--IAIK-----KEKRP--PQTLSRGWDQDLIWTQYEEGLFVAKSK 59

Qy 101 KPLMIHHLDECPSQALKKVFAPENKEIOKLAE--QFVLLNLVYETTDKHLSPDQGYVPRI 159

Db 60 KPLMIHHLDECQYSQALKKVFAPENKEIOQAQNKFMFLNLMHETTDKNLSPDQGYVPRI 119

Qy 160 MFVDPSTLVRADITGRYSNRLYAYEPADTALLDNMKKALKLKTTEL 206

Db 120 MFVDPSTLVRADITGRYSNRLYAYEPADTALLDNMKKALKLKTTEL 166

RESULT 6

US-08-916-576B-7

; Sequence 7, Application US/08916576B

; Patent No. 6171816

; GENERAL INFORMATION:

; APPLICANT: YU, GUO-LIANG

; APPLICANT: DILLON, PATRICK J.

; APPLICANT: EBNER, REINHARD

; APPLICANT: ENDRESS, GREGORY A.

; TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS

; NUMBER OF SEQUENCES: 45

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.

; STREET: 1100 NEW YORK AVENUE, SUITE 600

; CITY: WASHINGTON

; STATE: DC

; COUNTRY: US

; ZIP: 20005-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/916,576B

; FILING DATE:

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/024,347

; FILING DATE: 23-AUG-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: STEFFE, ERIC K.

; REGISTRATION NUMBER: 36,688

; REFERENCE/DOCKET NUMBER: 1488.0500001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 183 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-916-576B-7

Query Match

Best Local Similarity 42.1%; Score 448; DB 3; Length 183;

Mismatches 29; Conservative 29; Mismatches 51; Indels 10; Gaps 3;

Matches 88; Conservative 29; Mismatches 51; Indels 10; Gaps 3;

Qy 39 AFLLLVALSYTLARDTTVKP---GAKDXTKDSRPKLP-----QTLSRGWDQDLIWTQY 89

Db 6 SLVCLVLLCSALGEAVLKPKKQAGTTDTKTDQEPAPIKTKGLKTLDRGWSIEWQTY 65

Qy 90 EEALYKSKTSNKPLMIHHLDECPSQALKKVFAPENKEIOKLA-EQFVLLNLVYETTDK 148

```
Db 66 EBLAKARENKPMWHLHLEDCPSIALKKAFAVADRMQAQKLAQEDFIMNLVHPVADEN 125
QY 149 LSPDGOYVPRIMFVDSLTVRADITGRYSNRLYAYEPADTALLDNKKALKLLKTEL 206
Db 126 QSPDGHVPRVIFDPSLTVRSLDKRGYKMYAYDADDIPELITNKKAKSFLKTEL 183

RESULT 7
US-08-916-576B-4
; Sequence 4, Application US/08916576B
; Patent No. 6171816
; GENERAL INFORMATION:
; APPLICANT: YU, GUO-LIANG
; APPLICANT: DILLON, PATRICK J.
; APPLICANT: EBNER, REINHARD
; APPLICANT: ENDRESS, GREGORY A.
; TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916,576B
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/024,347
; FILING DATE: 23-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0500001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 172 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-916-576B-4

Query Match 20.9%; Score 222; DB 3; Length 172;
Best Local Similarity 34.2%; Pred. No. 1.4e-17;
Matches 54; Conservative 26; Mismatches 56; Indels 22; Gaps 3;

QY 66 DSRPKLPQT-----LSRGWGDQLIWTQTYEALYKSKTSKNPLMII 106
Db 2 ETRPRGLATCLGFSFLLLVSSDGHNLGKGFGDHIHW-RTLEDGKKAASGLPLMVI 60

QY 107 HHLDCHPSQALKKVFPAENKEIQKLAQFVLLN--VYETTDKHLSPDGOYVPRIMFVDP 164
Db 61 IHKSWCGACKALKPKFAESTEISELSHNFVMVNLDEEERPKDEDFSPDGGYIPIRLFLDP 120

QY 165 SLTVRADITGRYSNRLYAYEPADTALLDNKKALKLL 202
Db 121 SGKVHPEIINENGPNPSYKYFVVSABQVVGKMQAQL 158

RESULT 8
US-09-198-452A-1234
; Sequence 1234, Application US/09198452A
```

```
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1234
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; US-09-198-452A-1234

Query Match 8.3%; Score 88.5; DB 4; Length 118;
Best Local Similarity 24.6%; Pred. No. 0.018;
Matches 33; Conservative 29; Mismatches 45; Indels 27; Gaps 5;

QY 29 RVAMEKIPVSAFLLLVALSYYTLARTTVKPGAKKDTKDSRPKLQTLSRGWGDQLIWTQT 88
Db 9 RCLSKQLKVLATLL---LSLSL-----PTLEAENRDS-----DSIVVHLD 46

QY 89 YEALYKSKTSNKLPMIHHLDDEC--PHSQALKKVFPAENKEIQKLAQFVLLNLVYETTD 146
Db 47 YQALQKSKAEALPLLVIFSGSDWNGPCMKIRKEVLESPEFIKRVQGFVCEVEYL--- 103

QY 147 KHLSPDGOYVPRIM 160
Db 104 KHRPQLKTFVSKIL 117

RESULT 9
US-08-884-681-5
; Sequence 5, Application US/08884681
; Patent No. 5955338
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: NEW HUMAN PHOSPHATIDYLINOSITOL
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/884,681
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0334 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 901 amino acids
; TYPE: amino acid
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STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 1420920  
US-08-884-681-5

Query Match 7.7%; Score 81.5; DB 2; Length 901;  
Best Local Similarity 23.7%; Pred. No. 2.3;  
Matches 45; Conservative 32; Mismatches 46; Indels 67; Gaps 13;  
Qy 55 TVKFGAKKOTKDSRPK--LPQTLRSGWGDQLIWQTYYEAL-YKS-----KTS-NKPLMII 106  
Db 476 TYKYDSTDRWDSGKCRVP-----AWCDRLWRGTNVNQLYRSHMELKTSDHKPVSA 530  
Qy 107 HHL-----DECPHQAQKKVFAENKEIQKLAEE-----QFVLLNLVYETTDK-- 147  
Db 531 FHIGVKVUDE-----RRYRKVFEDSVRIMDRMENDFLPSLELSRREFVFNKFRLOQK 586  
Qy 148 -HLSPDGQ-----YVPRIM-----FVDPSTVTRADITGRYSNRLYAYE 184  
Db 587 FQISNNGQVPCHFSPFKLNDQYCKPWLRAEPFEGYLEPNETV--DIS-----LDVYV 638  
Qy 185 PADTALLDN 194  
Db 639 SKDSVTILNS 648

RESULT 10  
US-09-258-643-5  
; Sequence 5, Application US/09258643  
; Patent No. 6277373  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Lal, Preeti  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: NEW HUMAN PHOSPHATIDYLINOSITOL  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/258,643  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/884,681  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0334 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 901 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 1420920

US-09-258-643-5

Query Match 7.7%; Score 81.5; DB 3; Length 901;  
Best Local Similarity 23.7%; Pred. No. 2.3;  
Matches 45; Conservative 32; Mismatches 46; Indels 67; Gaps 13;  
Qy 55 TVKFGAKKOTKDSRPK--LPQTLRSGWGDQLIWQTYYEAL-YKS-----KTS-NKPLMII 106  
Db 476 TYKYDSTDRWDSGKCRVP-----AWCDRLWRGTNVNQLYRSHMELKTSDHKPVSA 530  
Qy 107 HHL-----DECPHQAQKKVFAENKEIQKLAEE-----QFVLLNLVYETTDK-- 147  
Db 531 FHIGVKVUDE-----RRYRKVFEDSVRIMDRMENDFLPSLELSRREFVFNKFRLOQK 586  
Qy 148 -HLSPDGQ-----YVPRIM-----FVDPSTVTRADITGRYSNRLYAYE 184  
Db 587 FQISNNGQVPCHFSPFKLNDQYCKPWLRAEPFEGYLEPNETV--DIS-----LDVYV 638  
Qy 185 PADTALLDN 194  
Db 639 SKDSVTILNS 648

RESULT 11  
US-08-560-005-7  
; Sequence 7, Application US/08560005  
; Patent No. 6001354  
; GENERAL INFORMATION:  
; APPLICANT: Pot, David A.  
; APPLICANT: Williams, Lewis T.  
; APPLICANT: Jefferson, Anne Bennett  
; APPLICANT: Majerus, Philip W.  
; TITLE OF INVENTION: No. 6001354el Grb2 Associating Protein and Nucleic  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/560,005  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dow, Karen B.  
; REGISTRATION NUMBER: 29,684  
; REFERENCE/DOCKET NUMBER: 2307K-0624000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-328-2422  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 968 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 1..968  
; OTHER INFORMATION: /note= "ocr1"  
US-08-560-005-7

Query Match 7.7%; Score 81.5; DB 3; Length 968;  
Best Local Similarity 23.7%; Pred. No. 2.6;  
Matches 45; Conservative 32; Mismatches 46; Indels 67; Gaps 13;

55	QY	TVKPGAKDITKDSRPK--LPOTLSRGWGDLITQTVEEAL--YKS-----KTS-NKPLMLI 106
551	Db	TVKYDSKTDKRWDSGKCRVP-----AMCDRLMRGTNVNQLVNRSHMLLXKTSDHKPVSAI 605
107	QY	HHL-----DECPSQALKKVFPAENKEIQKLAEE-----QFVLLNLVYETTDK-- 147
606	Db	PHIGVKWVDE----RRYRKVPEDSVRINDRMENDFLPSLELSRRFEFVFNKVRQLOQKG 661
148	QY	HLSPDQG-----YVPRIM-----FWDPSLTVRAIDITGRYSNRLYAYE 184
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185	QY	PADTALLDN 194
714	Db	SKDSVTLNS 723

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RESULT 12
US-09-418-540-7
: Sequence 7, Application US/09418540
: Patent No. 6296848
: GENERAL INFORMATION:
: APPLICANT: Pot, David A.
: APPLICANT: Williams, Lewis T.
: APPLICANT: Jefferson, Anne Bennett
: APPLICANT: Majerus, Philip W.
: TITLE OF INVENTION: No. 6296848e1 Grb2 Associating Protein and Nucleic
: TITLE OF INVENTION: Acids Encoding Therefor
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew
: STREET: One Market Plaza, Steuart Tower, Suite 2000
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94105
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0. Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/418,540
: FILING DATE: 14-OCT-1999
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/560,005
: FILING DATE: 17-NOV-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Dow, Karen B.
: REGISTRATION NUMBER: 29,684
: REFERENCE/DOCKET NUMBER: 2307K-0624000
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-326-2400
: TELEFAX: 415-326-2422
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 968 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FEATURE:
: NAME/KEY: Region
: LOCATION: 1..968
: OTHER INFORMATION: /note= "ocr1"
US-09-418-540-7

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RESULT 14  
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; Sequence 998 Application US/09198452A  
; Patent No. 6559294  
; GENERAL INFORMATION:  
; APPLICANT: Griffais, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments  
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention  
; TITLE OF INVENTION: and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/09/198,452A  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 998  
; LENGTH: 166  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
US-09-198-452A-998

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Db 10 FCRLSAIDFTLLCCT--KTCFWRNLQOTRPIAANLQ-----W-ESYAEALHSKQD 58  
QY 100 NKPL-MIIHLDCEPHSAKVKVFAENKEIQKLAEQFVLLNLV-----YETTDK 147  
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QY 148 HLSPDGQY-----VPRIMFVDPSTVTRADITGRYSNRLYAYEPADTALLDNKKALKL 201  
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RESULT 15  
US-09-534-638-5  
; Sequence 5, Application US/09534638  
; Patent No. 6320038  
; GENERAL INFORMATION:  
; APPLICANT: Panula, Pertti A.J.  
; APPLICANT: Brandt, Annika  
; APPLICANT: Westerlund, Johanna  
; TITLE OF INVENTION: Promoter for Neuropeptide FF Promoter and use thereof  
; TITLE OF INVENTION: for therapy and diagnosis  
; FILE REFERENCE: 2530-104  
; CURRENT APPLICATION NUMBER: US/09/534,638  
; CURRENT FILING DATE: 2000-03-27  
; EARLIER APPLICATION NUMBER: 09/365755  
; EARLIER FILING DATE: 1999-08-03  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 129  
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Query Match 7.3%; Score 78; DB 4; Length 129;  
Best Local Similarity 22.9%; Pred. No. 0.34;  
Matches 16; Conservative 14; Mismatches 40; Indels 0; Gaps 0;  
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QY 104 MIIHLDCEP 113  
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Search completed: November 26, 2003, 15:56:59  
Job time : 22 secs

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 30, 2003, 02:24:26 ; Search time 64 Seconds  
(without alignments)  
1420.702 Million cell updates/sec

Title: US-09-674-266A-181  
Perfect score: 1063  
Sequence: 1 RLSCAGTSGSGPHSPRLT.....DTALLDNMKKALKLLKTEL 206

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-MODEL=frame+ p2n.model -DEV=xlh  
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Database : Issued Patents NA:  
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6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	991	93.2	875	3 US-08-916-576B-1	Sequence 1, Appli
2	961	90.4	1689	4 US-09-247-155-61	Sequence 61, Appl
3	914	86.0	940	4 US-09-247-155-149	Sequence 149, App
4	856.5	80.6	793	3 US-09-040-984-78	Sequence 78, Appl
5	856.5	80.6	793	4 US-09-123-912-78	Sequence 78, Appl
6	856.5	80.6	793	4 US-09-643-597-78	Sequence 78, Appl
7	856.5	80.6	793	4 US-09-480-884A-78	Sequence 78, Appl
8	856.5	80.6	793	4 US-09-542-615A-78	Sequence 78, Appl
9	856.5	80.6	793	4 US-09-606-421B-78	Sequence 78, Appl
10	683	64.3	401	3 US-09-221-298-32	Sequence 32, Appl
11	642	60.4	386	3 US-08-916-576B-35	Sequence 35, Appl
12	631	59.4	404	4 US-09-643-597-282	Sequence 282, App

13	631	59.4	404	4	US-09-480-884A-282	Sequence 282, App
14	631	59.4	404	4	US-09-542-615A-282	Sequence 282, App
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16	555	52.2	732	3	US-08-916-576B-5	Sequence 5, Appl
17	547	51.5	321	4	US-09-389-681-218	Sequence 218, App
18	547	51.5	321	4	US-09-620-405B-218	Sequence 218, App
19	547	51.5	321	4	US-09-339-338-218	Sequence 218, App
20	547	51.5	321	4	US-09-433-826B-218	Sequence 218, App
21	547	51.5	321	4	US-09-604-287A-218	Sequence 218, App
22	487.5	45.9	373	3	US-08-916-576B-36	Sequence 36, Appl
23	458.5	43.1	489	3	US-08-916-576B-9	Sequence 9, Appl
24	384	36.1	235	4	US-09-702-705-410	Sequence 410, App
25	384	36.1	235	4	US-09-736-457-410	Sequence 410, App
26	376.5	35.4	506	3	US-08-916-576B-10	Sequence 10, Appl
27	266	25.0	198	4	US-09-702-705-1183	Sequence 1183, Ap
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31	253	23.8	158	3	US-08-916-576B-37	Sequence 37, Appl
32	252	23.7	159	4	US-09-030-607-209	Sequence 209, App
33	252	23.7	159	4	US-09-439-313-209	Sequence 209, App
34	252	23.7	159	4	US-09-352-616A-209	Sequence 209, App
35	252	23.7	159	4	US-09-232-149A-209	Sequence 209, App
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37	237	22.3	171	4	US-09-620-405B-412	Sequence 412, App
38	237	22.3	171	4	US-09-433-826B-412	Sequence 412, App
39	237	22.3	171	4	US-09-604-287A-412	Sequence 412, App
40	222	20.9	1423	3	US-08-916-576B-3	Sequence 3, Appl
41	183.5	17.3	136	3	US-08-916-576B-38	Sequence 38, Appl
42	158	14.9	302	3	US-08-916-576B-19	Sequence 19, Appl
43	147.5	13.9	310	3	US-08-916-576B-41	Sequence 41, Appl
44	129	12.1	311	3	US-08-916-576B-40	Sequence 40, Appl
45	104	9.8	329	3	US-08-916-576B-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-08-916-576B-1  
; Sequence 1, Application US/08916576B  
; Patent No. 6171816  
; GENERAL INFORMATION:  
; APPLICANT: YU, GUO-LIANG  
; APPLICANT: DILLON, PATRICK J.  
; APPLICANT: EBER, REINHARD  
; APPLICANT: ENDRESS, GREGORY A.  
; TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 NEW YORK AVENUE, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: US  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/916,576B  
; FILING DATE:  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/024,347  
; FILING DATE: 23-AUG-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0500001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600

Mon Dec 1 13:38:28 2003

118-09-674-266a-181.rni

TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 875 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 71..595  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 131..595  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 71..130  
-08-08-916-576B-1

Alignment Scores:	5.89e-117	Length:	875
Ordered No.:	991.00	Matches:	193
Score:	99.48%	Conservative:	0
Percent Similarity:	99.48%	Mismatches:	1
Best Local Similarity:	93.23%	Indels:	0
Query Match:	3	Gaps:	0
JB:			

US-08-574-266A-1A1 (1-206) x US-08-916-576B-1 (1-875)

13	ProHisProSerArgArgLeuThrGlnGlyArgTrpValArgLysSerArgValalaMet	32
14	CCGNATTCCTAGCCGCCGACTCACACAAGGCAGGTGGGTGAGGAAATCCAGAGTTGCCATG	73
33	GluLysIleProValSerAlaPheLeuLeuLeuValAlaLeuSerTyrThrLeuAlaArg	52
74	GAGAAAAATTCAGTGTCAGCATTTCTGCTCTTGTGGCCCTCTCTCTACACTCTGGCCAGA	133
53	AspThrThrValLysProGlyAlaValLysAspThrLysAspSerArgProLysLeuPro	72
134	GATACCACAGTCAAAACCTGGAGCAGCAAAAGGACACAAAGGACTCTCGACCCCAAACTGCC	193
73	GlnThrLeuSerArgGlyTrpGlyAspGlnLeuIleTrpThrGlnThrTyrGluGluAla	92
194	CAGACCCCTCTCCAGAGTTGGGGTGACCAACTCATCTGGACTCAGACATATGAAGAAGCT	253
93	LeuTyrLysSerLysThrSerAsnLysProLeuMetIleIleHisLeuAspGluCys	112
254	CTATATAAATCCAAAGACACAGCAACCAACCCCTTGATGATTATTATCATTGATGATGATGC	313
113	ProHisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIleGlnLysLeuAla	132
314	CCACACAGTCAGGCTTTTAAGAAAGTGTGTGCTGAAATAAAGAAATCCAGAAATTTGGCA	373
133	GluGlnPheValLeuLeuAsnLeuValTyrGluThrThrAspLysHisLeuSerProAsp	152
374	GAGCAGTTTGTCCTCCTCAATCTGGTTATGAAACAACTGACAAACACCTTTCTCTCGAT	433
153	GlyGlnTyrValProArgIleMetPheValAspProSerLeuThrValArgAlaAspIle	172
434	GGCCAGTATGTCCCCAGAGATTATGTTGTTGACCCCATCTCTGACAGTTAGAGCCGATATC	493
173	ThrGlyArgTyrSerAsnArgLeuTyrAlaTyrGluProAlaAspThrAlaLeuLeuLeu	192
494	ACTGGGAAGATATTCAAATCGTCTCATGCTTACGACCTGCAGATACAGCTCTGTGCTT	553
193	AspAsnMetLysLysAlaLeuLysLeuLeuLysThrGluLeu	206
554	GACCAATCATGAGAAAGCTCTCAAGTTGCTGAAGACTGAATTG	595

## RESULT 2

US-09-247-155-61  
; Sequence 61, Application US/09247155A  
; Patent No. 6312922

Qy 132 AlaGluGlnPheValLeuLeuAsnLeuValTyrGluThrThrAspLysHisLeuSerPro 151  
Db 351 GCAGAGCAGTTTGTCTCTCTCAATCTGTTTATGAAACAACTGACAAACACCTTTCTCT 410  
Qy 152 AspGlyGlnTyrValProArgGlyMetPheValAspProSerLeuThrValArgAlaAsp 171  
Db 411 GATGGCAGATGTCCTGAGATGTTGTTGACCCATCTCTGACAGTTAGAGCCGAT 470  
Qy 172 IleThrGlyArgTyrSerAsnArgLeuTyrAlaTyrGluProAlaAspThrAlaLeuLeu 191  
Db 471 ATCACTGGAAGATATTCAATCGTCTCTATGCTTACGAACCTCGAGATACAGCTCTGTTG 530  
Qy 192 LeuAspMetLysLysAlaLeuLysLeuLeuLysThrGluLeu 206  
Db 531 CTTGACAACTGGAAGAGCTCTCAAGTTGCTGAAGACTGAATTG 575

## RESULT 3

US-09-247-155-149  
; Sequence 149, Application US/09247155A  
; Patent No. 6312922

## ; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Bouquelere, Lydie

; TITLE OF INVENTION: Complementary DNAs  
; FILE REFERENCE: GENSET.021A  
; CURRENT APPLICATION NUMBER: US/09/247,155A

; EARLIER FILING DATE: 1999-02-09

; EARLIER APPLICATION NUMBER: 60/074,121

; EARLIER FILING DATE: 1998-02-09

; EARLIER FILING DATE: 1998-04-13

; EARLIER FILING DATE: 1998-08-10

; EARLIER APPLICATION NUMBER: 60/096,116

; EARLIER FILING DATE: 1998-10-04

; NUMBER OF SEQ ID NOS: 182

; SOFTWARE: Patent.pm

; SEQ ID NO 149

; LENGTH: 940

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 177..569

; FEATURE:

; NAME/KEY: sig\_peptide

; LOCATION: 177..236

; OTHER INFORMATION: Von Heijne matrix

; OTHER INFORMATION: score 11.1999998092651

; OTHER INFORMATION: seq AFLLLVALSYTLA/RD

; FEATURE:

; NAME/KEY: polyA\_site

; LOCATION: 931..939

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: 482

; OTHER INFORMATION: n=a, g, c o r t

US-09-247-155-149

## Alignment Scores:

Pred. No.: 5.15e-107 Length: 940  
Score: 914.00 Matches: 188  
Percent Similarity: 90.82% Conservative: 0  
Best Local Similarity: 90.82% Mismatches: 12  
Query Match: 85.98% Indels: 8  
DB: 4 Gaps: 1

US-09-674-266A-181 (1-206) x US-09-247-155-149 (1-940)

Qy 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgArgLeuThr 20  
Db 103 AGACTCAGCTGTGTGTCACATCAGAAGCTT-GGACCGCATCTCGCCGCGACTCACA 161

Qy 21 GlnGlyArgTrpValArgLysSerArgValAlaMetGluLysIleProValSerAlaPhe 40  
Db 162 CAAGGC-----AGAGTTGCCATGGAAAAAATTCAGTGTTCAGCATTC 203  
Qy 41 LeuLeuLeuValAlaLeuSerTyrThrLeuAlaArgAspThrThrValLysProGlyAla 60  
Db 204 TTCTCTCTTTGTGGCCCTCTCTCACTCTGGCCAGAGATACACACAGTCAACCTGGAGCC 263  
Qy 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTTrpGly 80  
Db 264 AAAAGAGACACAAGAGACTCTCGACCCAAACTCCCCAGACCTCTCCAGAGTTGGGGT 323  
Qy 81 AspGlnLeuIleTrpThrGlnThrTyrGluGluAlaLeuTyrLysSerLysThrSerAsn 100  
Db 324 GACCAACTCATCTGGACACACACATATGAARAARCTCTATWTAAATCCAAACAAGCAAC 383  
Qy 101 LysProLeuMetIleIleHisLeuAspGluCysProHisSerGlnAlaLeuLysLys 120  
Db 384 AAACCCCTTGATGATTATTTCATCACTTGGATGADTGGCCACACACAGTCAAGCTTTAAAAAAA 443  
Qy 121 ValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluGlnPheValLeuLeuAsnLeu 140  
Db 444 KTGTGTTGCTGAAATAAARAAATCCAGAAATGGCARANCAAGTTTGTCTCCCTCAATCTG 503  
Qy 141 ValTyrGluThrThrAspLysHisLeuSerProAspGlyGlnTyrVal-ProArgIleMe 160  
Db 504 GTTTATGAAACAACACTGACAAACACCTTTCTCTGTATGGCCAATATATKCCCCCGGATTAT 563  
Qy 160 tPheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnArgLe 180  
Db 564 GTTTGTTGACCCATCTCTGACAGTTAGAGCCGATATCACTGGAGATATTTCAAAAYCGTCT 623  
Qy 180 uTyrAlaTyrGluProAlaAspThrAlaLeuLeuAspAsnMetIysLysAlaLeuLy 200  
Db 624 CTAAGCTTACGAACCTGCGAGATACAGTCTGTGTGTTGACAAATGATGAAGAAAGCTCTCAA 683  
Qy 200 sLeuLeuLysThrGluLeu 206  
Db 684 GTTGCTGAAGACTGAATTG 702

## RESULT 4

US-09-040-984-78

; Sequence 78, Application US/09040984

; Patent No. 6210883

; GENERAL INFORMATION:

; APPLICANT: Reed, Steven G.

; APPLICANT: Wang, Tongtong

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS

; TITLE OF INVENTION: OF LUNG CANCER

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SEED and BERRY LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/040,984

; FILING DATE: 18-MAR-1998

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Maki, David J.

; REGISTRATION NUMBER: 31,392

; REFERENCE/DOCKET NUMBER: 210121.456

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-622-4900

```
; TELEFAX: 206-282-6031
; TELEX:
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 793 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-040-984-78

Alignment Scores:
Pred. No.: 8.57e-100 Length: 793
Score: 856.50 Matches: 177
Percent Similarity: 94.74% Conservative: 3
Best Local Similarity: 93.16% Mismatches: 9
Query Match: 80.57% Indels: 3
DB: Gaps: 1

US-09-674-266A-181 (1-206) x US-09-040-984-78 (1-793)

QY 14 HisProSerArgGlyLeuThrGlnGlyArgTTPValArgLysSerArgValAlaMetGlu 33
Db 2 CATCTAGCGCGGACTCACAAGGCGAGTGGTGAGGAAATCCAGAGTTGCCATGGAG 61
QY 34 LysIleProValSerAlaPheLeuLeuValAlaLeuSerTyrThrLeuAlaArgAsp 53
Db 62 AAAATTCAGTGTACAGATTCCTCTTGCGCCCTCTCTACACTCTGCCAGAGAT 121
QY 54 ThrThrValLysProGlyAlaLysLysAspThrLysAspSerArgProLysLeuProGln 73
Db 122 ACCACAGTCAAACTGGAGCGCAAAAGGACACAAAGGACTCTCGACCCAACTGCCCCAG 181
QY 74 ThrLeuSerArgGlyTTPGlyAspGlnLeuIleTTPThrGlnThrTyrGluAlaLeu 93
Db 182 ACCCTCTCAGAGTTGGGTGACCAACTCATCTGGACTCAGACATATGAAGAAGCTTA 241
QY 94 TyrLysSerLysThrSerAsnLysProLeuMetIleIleHisLeuAspGluCysPro 113
Db 242 TATAATCCAGACAGCAACAAACCTTGATGATTATTCATCATTGGATGATGCCCA 301
QY 114 HisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIleGlnLysLeuAlaGlu 133
Db 302 CACAGTCNAGCTTTAAAGAAAGTGTCTGCTGAAAATAAAGAAATCCAGAAATGGCAGAG 361
QY 134 GlnPheValLeuLeuAsnLysValTyrGluThrThrAspLysHisLeuSerProAspGly 153
Db 362 CAGTTTGTCTCTCAATCTGGTTATGAACAACACTGACAAACACCTTTCTCTGATGC 421
QY 154 GlnTyrValProArgIleMetPheValAspProSerLeuThrValArgAlaAspIleThr 173
Db 422 CAGTATGT-CCAGGATTAATGTTTGTGACCCCATCTCTACAGTTGAAGCCGATATCCTG 480
QY 174 GlyArgTyrSerAsnArgLeuTyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAsp 193
Db 481 GGAAGATATTCAACCGTCTCTATGCTTACAAACT-GCAGATACGCTCTGTTGCTTGACA 539
QY 194 AsnMetLysLysAlaLeuLysLeuLys 203
Db 540 CAT---GNAAGAGCTCTCAAGTTGCTNAA 566

RESULT 5
US-09-123-912-78
; Sequence 78, Application US/09123912A
; Patent No. 6312695
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
; FILE REFERENCE: 210121.455C1
; CURRENT APPLICATION NUMBER: US/09/123,912A
; CURRENT FILING DATE: 1998-07-27
; PRIOR FILING DATE: 09/040,802
; PRIOR FILING DATE: 1998-03-18
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; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
; LENGTH: 793
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (309)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (492)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (563)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (657)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (660)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (703)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (708)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (710)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (711)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (732)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (740)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (748)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (758)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (762)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (765)
; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (787)
; OTHER INFORMATION: Where n is a, c, g or t
US-09-123-912-78

Alignment Scores:
Pred. No.: 8.57e-100 Length: 793
Score: 856.50 Matches: 177
Percent Similarity: 94.74% Conservative: 3
Best Local Similarity: 93.16% Mismatches: 9
Query Match: 80.57% Indels: 3
DB: Gaps: 1

US-09-674-266A-181 (1-206) x US-09-123-912-78 (1-793)

QY 14 HisProSerArgGlyLeuThrGlnGlyArgTTPValArgLysSerArgValAlaMetGlu 33
Db 2 CATCTAGCGCGGACTCACAAGGCGAGTGGTGAGGAAATCCAGAGTTGCCATGGAG 61
QY 34 LysIleProValSerAlaPheLeuLeuValAlaLeuSerTyrThrLeuAlaArgAsp 53
```

Db 62 AAAATTCAGTGTGAGCATTTCTGCTCTTGGCCCTCTCTACACTCTGGCCAGAGAT 121  
 Qy 54 ThrThrValLysProGlyAlaLysLysAspThrLysAspSerArgProLysLeuProGln 73  
 Db 122 ACCACAGTCAAACTGGAGCCAAAGGACACAAAGGACTCTCGACCAAACTGCCCCAG 181  
 Qy 74 ThrLeuSerArgGlyTrpGlyAspGlnLeuLeuLeuLeuLeuLeuLeuLeuLeu 93  
 Db 182 ACCCTCTCCAGAGGTGGGGTGAGCAACTCATCTGGACTCAGACATATGAAGAAGCTCTA 241  
 Qy 94 TyrLysSerLysThrSerAsnLysProLeuMetIleIleHisLysLeuAspGluCysPro 113  
 Db 242 TATTAATCCAGACAGCAAAACCTTTGATGATTATTCATCACTTGGAGTGGCCCA 301  
 Qy 114 HisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIleGlnLysLeuAlaGlu 133  
 Db 302 CACAGTCNAGCTTTAAAGAAAGTGTTCCTGAAATAAAGAAATCCAGAAATGGCAGAG 361  
 Qy 134 GlnPheValLeuLeuAsnLeuValTyrgluThrThrAspLysHisLeuSerProAspGly 153  
 Db 362 CAGTTTGTCTCTCAATCTGGTTTATGAACAACCTGACCACTCTCGACAGTTGAAGCGGATATCTG 421  
 Qy 154 GlnTyrrValProArgIleMetPheValAspProSerLeuThrValAlaAspIleThr 173  
 Db 422 CAGTATGT-CCAGGATTATGTTGTGACCCACTCTCGACAGTTGAAGCGGATATCTG 480  
 Qy 174 GlyArgTyrrSerAsnArgLeuTyrrAlaTyrgluProAlaAspThrAlaLeuLeuLeuAsp 193  
 Db 481 GGAAGATATTCNAACCGTCTCTATGCTTACAACT-CCAGATACGCTCTGTTGCTTGACA 539  
 Qy 194 AsnMetLysLysAlaLeuLysLeuLeuLys 203  
 Db 540 CAT---GAAAAAGCTCTCAAGTTGCTNAAA 566

## RESULT 6

US-09-643-597-78

; Sequence 78, Application US/09643597

; Patent No. 6426072

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy

; APPLICANT: Fanger, Gary R.

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Henderson, Robert A.

; APPLICANT: McNeill, Patricia D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.455C11

; CURRENT APPLICATION NUMBER: US/09/643,597

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 78

; LENGTH: 793

; TYPE: DNA

; ORGANISM: Homo sapien

; NAME/KEY: misc feature

; LOCATION: (1)-(793)

; OTHER INFORMATION: n = A, T, C or G

US-09-643-597-78

Alignment Scores:

Pred. No.: 8.57e-100 Length: 793

Score: 856.50 Matches: 177

Percent Similarity: 94.74% Conservative: 3

Best Local Similarity: 93.16% Mismatches: 9

Query Match: 80.57% Indels: 3

DB: 4 Gaps: 1  
 US-09-674-266A-181 (1-206) x US-09-643-597-78 (1-793)  
 Qy 14 HisProSerArgArgLeuThrGlnGlyArgTrpValArgLysSerArgValAlaMetGlu 33  
 Db 2 CATCTTAGCCCGCAGACTCACAAAGGAGGTGGGTGAGGAAATCCAGAGTTGCCATGGAG 61  
 Qy 34 LysIleProValSerAlaPheLeuLeuValAlaLeuSerTyrrThrLeuAlaAsp 53  
 Db 62 AAAATTCAGTGTGAGCATTTCTGCTCTTGGCCCTCTCTACACTCTGGCCAGAGAT 121  
 Qy 54 ThrThrValLysProGlyAlaLysLysAspThrLysAspSerArgProLysLeuProGln 73  
 Db 122 ACCACAGTCAAACTGGAGCCAAAGGACACAAAGGACTCTCGACCAAACTGCCCCAG 181  
 Qy 74 ThrLeuSerArgGlyTrpGlyAspGlnLeuLeuLeuLeuLeuLeuLeuLeuLeu 93  
 Db 182 ACCCTCTCCAGAGGTGGGGTGAGCAACTCATCTGGACTCAGACATATGAAGAAGCTCTA 241  
 Qy 94 TyrLysSerLysThrSerAsnLysProLeuMetIleIleHisLysLeuAspGluCysPro 113  
 Db 242 TATTAATCCAGACAGCAAAACCTTTGATGATTATTCATCACTTGGAGTGGCCCA 301  
 Qy 114 HisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIleGlnLysLeuAlaGlu 133  
 Db 302 CACAGTCNAGCTTTAAAGAAAGTGTTCCTGAAATAAAGAAATCCAGAAATGGCAGAG 361  
 Qy 134 GlnPheValLeuLeuAsnLeuValTyrgluThrThrAspLysHisLeuSerProAspGly 153  
 Db 362 CAGTTTGTCTCTCAATCTGGTTTATGAACAACCTGACCACTCTCGACAGTTGAAGCGGATATCTG 421  
 Qy 154 GlnTyrrValProArgIleMetPheValAspProSerLeuThrValAlaAspIleThr 173  
 Db 422 CAGTATGT-CCAGGATTATGTTGTGACCCACTCTCGACAGTTGAAGCGGATATCTG 480  
 Qy 174 GlyArgTyrrSerAsnArgLeuTyrrAlaTyrgluProAlaAspThrAlaLeuLeuLeuAsp 193  
 Db 481 GGAAGATATTCNAACCGTCTCTATGCTTACAACT-CCAGATACGCTCTGTTGCTTGACA 539  
 Qy 194 AsnMetLysLysAlaLeuLysLeuLeuLys 203  
 Db 540 CAT---GAAAAAGCTCTCAAGTTGCTNAAA 566

## RESULT 7

US-09-480-884A-78

; Sequence 78, Application US/09480884A

; Patent No. 6482597

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Hosken, Nancy A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.455C6

; CURRENT APPLICATION NUMBER: US/09/480,884A

; CURRENT FILING DATE: 2001-08-27

; NUMBER OF SEQ ID NOS: 330

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 78

; LENGTH: 793

; TYPE: DNA

; ORGANISM: Homo sapien

; NAME/KEY: misc feature

; LOCATION: (1)-(793)

; OTHER INFORMATION: n = A, T, C or G

US-09-480-884A-78

Alignment Scores:

Pred. No.: 8.57e-100 Length: 793

```
Score: 856.50 Matches: 177
Percent Similarity: 94.74% Conservative: 3
Best Local Similarity: 93.16% Mismatches: 9
Query Match: 80.57% Indels: 3
DB: 4 Gaps: 1

US-09-674-266A-181 (1-206) x US-09-480-884A-78 (1-793)

QY 14 HisProSerArgLeuThrGlnGlyArgTTPValArgLysSerArgValAlaMetGlu 33
DB 2 CATCTTAGCCCGGACTCACACAGGCGAGTGGTGGAGAAATCCAGAGTTGCCATGGAG 61
QY 34 LysileProValSerAlaPheLeuLeuValAlaLeuSerTyrThrLeuAlaArgAsp 53
DB 62 AAAATTCAGTGTTCAGCATTTCTGCTTGTGGCCCTCTCTACACTCTGGCCAGAT 121
QY 54 ThrThrValLysProGlyAlaLysLysAspThrLysAspSerArgProLysLeuProGln 73
DB 122 ACCACAGTCAAACTCGAGCCAAAAGGACACAAAGGACTCTCGACCCAACTGCCCCAG 181
QY 74 ThrLeuSerArgGlyTTPGlyAspGlnLeuLeuTTPThrGlnThrTyrGluGluAlaLeu 93
DB 182 ACCCTCTCCAGAGTGGGGTGACCACTCATCTGGACTCAGACATATGAAGAAGCTCTA 241
QY 94 TyrLysSerLysThrSerAsnLysProLeuMetIleIleHisHisLeuAspGluCysPro 113
DB 242 TATAATCCNAGACAGCAACAAACCTTGATGATTTATCATCTTGGATGGTCCCA 301
QY 114 HisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluLeuGlnLysLeuAlaGlu 133
DB 302 CACAGTCNAGCTTTAAAGAAAGTGTTCGTGAAAAATAAGAAATCCAGAAATGGCAGAG 361
QY 134 GlnPheValLeuLeuAsnLysValTyrGluThrThrAspLysHisLeuSerProAspGly 153
DB 362 CAGTTTGTCTCTCAATCTGTTTATGAACAACCTGCACAAACACCTTTCTCTGATGC 421
QY 154 GlnTyrValProArgIleMetPheValAspProSerLeuThrValArgAlaAspIleThr 173
DB 422 CAGTATGT-CCAGGATATGTTTGTGACCCATCTCTGACAGTTGAAGCCGATATCTTG 480
QY 174 GlyArgTyrSerAsnArgLeuTyrAlaTyrGluProAlaAspThrAlaLeuLeuAsp 193
DB 481 GGAAGATATTCAACCGCTCTCTATGCTTACAAACT-GCAGATACGCTCTGTTGCTTGACA 539

QY 194 AsnMetLysLysAlaLeuLysLeuLys 203
DB 540 CAT---GAAAAAGCTCTCAAGTTGCTNAAA 566

RESULT 8
US-09-542-615A-78
; Sequence 78, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy R.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT FILING DATE: 2000-04-14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 78
; LENGTH: 793
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(793)

; OTHER INFORMATION: n = A,T,C or G
US-09-542-615A-78
Alignment Scores:
Pred. No.: 8.57e-100 Length: 793
Score: 856.50 Matches: 177
Percent Similarity: 94.74% Conservative: 3
Best Local Similarity: 93.16% Mismatches: 9
Query Match: 80.57% Indels: 3
DB: 4 Gaps: 1

US-09-674-266A-181 (1-206) x US-09-542-615A-78 (1-793)

QY 14 HisProSerArgLeuThrGlnGlyArgTTPValArgLysSerArgValAlaMetGlu 33
DB 2 CATCTTAGCCCGGACTCACACAGGCGAGTGGTGGAGAAATCCAGAGTTGCCATGGAG 61
QY 34 LysileProValSerAlaPheLeuLeuValAlaLeuSerTyrThrLeuAlaArgAsp 53
DB 62 AAAATTCAGTGTTCAGCATTTCTGCTTGTGGCCCTCTCTACACTCTGGCCAGAT 121
QY 54 ThrThrValLysProGlyAlaLysLysAspThrLysAspSerArgProLysLeuProGln 73
DB 122 ACCACAGTCAAACTCGAGCCAAAAGGACACAAAGGACTCTCGACCCAACTGCCCCAG 181
QY 74 ThrLeuSerArgGlyTTPGlyAspGlnLeuLeuTTPThrGlnThrTyrGluGluAlaLeu 93
DB 182 ACCCTCTCCAGAGTGGGGTGACCACTCATCTGGACTCAGACATATGAAGAAGCTCTA 241
QY 94 TyrLysSerLysThrSerAsnLysProLeuMetIleIleHisHisLeuAspGluCysPro 113
DB 242 TATAATCCNAGACAGCAACAAACCTTGATGATTTATCATCTTGGATGGTCCCA 301
QY 114 HisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluLeuGlnLysLeuAlaGlu 133
DB 302 CACAGTCNAGCTTTAAAGAAAGTGTTCGTGAAAAATAAGAAATCCAGAAATGGCAGAG 361
QY 134 GlnPheValLeuLeuAsnLysValTyrGluThrThrAspLysHisLeuSerProAspGly 153
DB 362 CAGTTTGTCTCTCAATCTGTTTATGAACAACCTGCACAAACACCTTTCTCTGATGC 421
QY 154 GlnTyrValProArgIleMetPheValAspProSerLeuThrValArgAlaAspIleThr 173
DB 422 CAGTATGT-CCAGGATATGTTTGTGACCCATCTCTGACAGTTGAAGCCGATATCTTG 480
QY 174 GlyArgTyrSerAsnArgLeuTyrAlaTyrGluProAlaAspThrAlaLeuLeuAsp 193
DB 481 GGAAGATATTCAACCGCTCTCTATGCTTACAAACT-GCAGATACGCTCTGTTGCTTGACA 539

QY 194 AsnMetLysLysAlaLeuLysLeuLys 203
DB 540 CAT---GAAAAAGCTCTCAAGTTGCTNAAA 566

RESULT 9
US-09-606-421B-78
; Sequence 78, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
```

SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 78  
LENGTH: 793  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(793)  
OTHER INFORMATION: n = A,T,C or G  
US-09-606-421B-78

Alignment Scores:  
Pred. No.: 8.57e-100 Length: 793  
Score: 856.50 Matches: 177  
Percent Similarity: 94.74% Conservative: 3  
Best Local Similarity: 93.16% Mismatches: 9  
Query Match: 80.57% Indels: 3  
DB: 4 Gaps: 1

US-09-674-266A-181 (1-206) x US-09-606-421B-78 (1-793)

Qy 14 HisProSerArgArgLeuThrGlnGlyArgTyrValAlaGlySerArgValAlaMetGlu 33  
Db 2 CATCTAGCCGCGACTCACACAGGCGAGTGGGTGAGGAATCCAGATGGCCATGGAG 61  
Qy 34 LysileProValSerAlaPheLeuLeuValAlaLeuSerTyrThrLeuAlaAArgAsp 53  
Db 62 AAAATCCAGTGTCCAGCATCTTGCTCTGTGGCCCTCTCTACACTCTGGCCAGAT 121  
Qy 54 ThrThrValLysProGlyAlaLysLysAspThrLysAspSerArgProLysLeuProGln 73  
Db 122 ACCACAGTCAACCTCGAGGCGAAAGGACACAAAGGACTCTGACCAAACTGCCCCAG 181  
Qy 74 ThrLeuSerArgGlyTTPGlyAspGlnLeuLeuThrGlnThrTyrGluGluAlaLeu 93  
Db 182 ACCCTCTCCAGAGTGGGTGACCACTCATCTGGACTCAGACATATGAAGAAGCTCTA 241  
Qy 94 TyLysSerLysThrSerAsnLysProLeuMetIleIleHisLeuAspGluCysPro 113  
Db 242 TATAATCCAGACACAAACCTCTGATGATTATTCATCATCTGGATGAGTGCCCA 301  
Qy 114 HisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluLeuGlnLysLeuAlaGlu 133  
Db 302 CACAGTCNAGCTTTAAAGAAAGTGTGTGCTGAAATAAAGAAATCCAGAAATGGCAG 361  
Qy 134 GlnPheValLeuLeuLeuValTyrGluThrThrAspLysHisLeuSerProAspGly 153  
Db 362 CAGTTTCTCTCTCAATCTGGTTATGAACCAACTGACAAACACCTTTCTCTGATGGC 421  
Qy 154 GlnTyrValProArgIleMetPheValAspProSerLeuThrValAlaAlaAspIleThr 173  
Db 422 CAGTATGT-CCAGGATTATGTTGTGACCCATCTCTGACAGTTGAAGCCGATATCCTG 480  
Qy 174 GlyArgTyrSerAsnArgLeuTyrAlaTyrGluProAlaAspThrAlaLeuLeuAsp 193  
Db 481 GGAAGATATTCAACCGCTCTATGCTTACAACT-CCAGATACGCTCTGTGTTGACA 539  
Qy 194 AsnMetLysLysAlaLeuLysLeuLys 203  
Db 540 CAT---GAAAAAGCTCTCAAGTTGCTNAAA 566

RESULT 10

US-09-221-298-32  
Sequence 32, Application US/09221298  
Patent No. 6284241  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND DIAGNOSIS  
FILE REFERENCE: 210121.471  
CURRENT APPLICATION NUMBER: US/09/221,298  
CURRENT FILING DATE: 1998-12-23  
NUMBER OF SEQ ID NOS: 112

SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 32  
LENGTH: 401  
TYPE: DNA  
ORGANISM: Human  
US-09-221-298-32

Alignment Scores:  
Pred. No.: 4.05e-78 Length: 401  
Score: 683.00 Matches: 132  
Percent Similarity: 98.51% Conservative: 0  
Best Local Similarity: 98.51% Mismatches: 1  
Query Match: 64.25% Indels: 1  
DB: 3 Gaps: 0

US-09-674-266A-181 (1-206) x US-09-221-298-32 (1-401)

Qy 57 LysProGlyAlaLysLysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSer 76  
Db 2 AAACCTGGAGCCCAAAAGGACACAAAGGACTCTCGACCAAACTGCCCCAGACCTCTCC 61  
Qy 77 ArgGlyTyrGlyAspGlnLeuIleTyrThrGlnThrTyrGluGluAlaLeuTyrLysSer 96  
Db 62 AGAGGTGGGGTGACCAACTCATCTGACTCAGACATATGAAGAAGCTCTATATAATCC 121  
Qy 97 LysThrSerAsnLysProLeuMetIleIleHisLeuAspGluCysProHisSerGln 116  
Db 122 AAGACAGACACAAACCTTGATGATTATTCATCTGGGTGAGTGCCACACAGTCAA 181  
Qy 117 AlaLeuLysLysValPheAlaGluAsnLysGluLeuGlnLysLeuAlaGluGlnPheVal 136  
Db 182 GCTTTAAAGAAAGTGTGTGCTGAAATAAAGAAATCCAGAAATGGCAGAGCAGTTTGT 241  
Qy 137 LeuLeuAsnLeuValTyrGluThrThrAspLysHisLeuSerProAspGlyGlnTyrVal 156  
Db 242 CTCTCAATCTGGTTATGAACCAACTGACAAACACCTTTCTCTGATGCCAGTATGTC 301  
Qy 157 ProArgIleMetPheValAspProSerLeuThrValAlaAla-AspIleThrGlyArgTy 176  
Db 302 CCAGGATTATGTTGTGACCCATCTCTGACAGTTAGAGCCCGATATCACTGGAAGNTA 361

RESULT 11

US-08-916-576B-35  
Sequence 35, Application US/08916576B  
Patent No. 6171816  
GENERAL INFORMATION:  
APPLICANT: YU, GUO-LIANG  
APPLICANT: DILLON, PATRICK J.  
APPLICANT: EBER, REINHARD  
APPLICANT: ENDRESS, GREGORY A.  
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 NEW YORK AVENUE, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: US  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/916,576B  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:





TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)-(404)  
OTHER INFORMATION: n = A,T,C or G  
US-09-674-266A-181

Alignment Scores:  
Pred. No.: 1.77e-71 Length: 404  
Score: 631.00 Matches: 125  
Percent Similarity: 92.59% Conservative: 0  
Best Local Similarity: 92.59% Mismatches: 4  
Query Match: 59.36% Indels: 6  
DB: 4 Gaps: 1

US-09-674-266A-181 (1-206) x US-09-480-884A-282 (1-404)

```
Qy 13 ProHisProSerArgArgLeuThrGlnGlyArgTrpValArgLysSerArgValAlaMet 32
Db 16 CCGCATCTTANNCCGCGACTCACACAAGC-----AGAGTNGCCATG 57
Qy 33 GlulysileProValSerAlaPheLeuLeuValAlaLeuSerTyrThrLeuAlaArg 52
Db 58 GAGAAATTCAGTGTCCAGTCTTCTCTCTTGTGGCCCTCTCTACACTCTGGCCAGA 117
Qy 53 AspThrThrValLysProGlyAlaLysLysAspThrLysAspSerArgProLysLeuPro 72
Db 118 GATACACAGTCAAACTGNAGCCAAAGAGACACAAAGGACTCTGACCCAAACTGCC 177
Qy 73 GlnThrLeuSerArgGlyTrpGlyAspGlnLeuLeuTrpThrGlnThrTyrGluGluAla 92
Db 178 CANACCTCTCCAGAGTGGGTGACCAACTCATCTGGACTCANACATATGAAGAAGCT 237
Qy 93 LeuTyrLysSerLysThrSerAsnLysProLeuMetIleHisLeuAspGluCys 112
Db 238 CTATATAATCCAGACAGCAACAAACCTTTGATGATTATTCATCACTTTGGATGAGTGC 297
Qy 113 ProHisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIleGlnLysLeuAla 132
Db 298 CCACAGTCNAGCTTTAAGAAAGTGTTCGTAATAAAGAAATCCAGAAATTTGGCA 357
Qy 133 GluGlnPheValLeuLeuAsnLeuValTyrGluThrThrAspLys 147
Db 358 GAGCAGTTTGTCTCTCAATCTGGTTTATGAAACAACACTGACAAA 402
```

## RESULT 14

US-09-542-615A-282  
Sequence 282, Application US/09542615A  
Patent No. 6518256  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy A.  
APPLICANT: Fanger, Gary R.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C8  
CURRENT APPLICATION NUMBER: US/09/542.615A  
CURRENT FILING DATE: 2000-04-14  
NUMBER OF SEQ ID NOS: 350  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 282  
LENGTH: 404  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)...(404)  
OTHER INFORMATION: n = A,T,C or G  
US-09-542-615A-282

## Alignment Scores:

Pred. No.: 1.77e-71 Length: 404  
Score: 631.00 Matches: 125  
Percent Similarity: 92.59% Conservative: 0  
Best Local Similarity: 92.59% Mismatches: 4  
Query Match: 59.36% Indels: 6  
DB: 4 Gaps: 1

US-09-674-266A-181 (1-206) x US-09-542-615A-282 (1-404)

```
Qy 13 ProHisProSerArgArgLeuThrGlnGlyArgTrpValArgLysSerArgValAlaMet 32
Db 16 CCGCATCTTANNCCGCGACTCACACAAGC-----AGAGTNGCCATG 57
Qy 33 GlulysileProValSerAlaPheLeuLeuValAlaLeuSerTyrThrLeuAlaArg 52
Db 58 GAGAAATTCAGTGTCCAGTCTTCTCTCTTGTGGCCCTCTCTACACTCTGGCCAGA 117
Qy 53 AspThrThrValLysProGlyAlaLysLysAspThrLysAspSerArgProLysLeuPro 72
Db 118 GATACACAGTCAAACTGNAGCCAAAGAGACACAAAGGACTCTGACCCAAACTGCC 177
Qy 73 GlnThrLeuSerArgGlyTrpGlyAspGlnLeuLeuTrpThrGlnThrTyrGluGluAla 92
Db 178 CANACCTCTCCAGAGTGGGTGACCAACTCATCTGGACTCANACATATGAAGAAGCT 237
Qy 93 LeuTyrLysSerLysThrSerAsnLysProLeuMetIleHisLeuAspGluCys 112
Db 238 CTATATAATCCAGACAGCAACAAACCTTTGATGATTATTCATCACTTTGGATGAGTGC 297
Qy 113 ProHisSerGlnAlaLeuLysLysValPheAlaGluAsnLysGluIleGlnLysLeuAla 132
Db 298 CCACAGTCNAGCTTTAAGAAAGTGTTCGTAATAAAGAAATCCAGAAATTTGGCA 357
Qy 133 GluGlnPheValLeuLeuAsnLeuValTyrGluThrThrAspLys 147
Db 358 GAGCAGTTTGTCTCTCAATCTGGTTTATGAAACAACACTGACAAA 402
```

## RESULT 15

US-09-606-421B-282  
Sequence 282, Application US/09606421B  
Patent No. 6531315  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy  
APPLICANT: Fanger, Gary R.  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C9  
CURRENT APPLICATION NUMBER: US/09/606.421B  
CURRENT FILING DATE: 2000-06-28  
NUMBER OF SEQ ID NOS: 358  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 282  
LENGTH: 404  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)...(404)  
OTHER INFORMATION: n = A,T,C or G  
US-09-606-421B-282

## Alignment Scores:

Pred. No.: 1.77e-71 Length: 404  
Score: 631.00 Matches: 125

Percent Similarity: 92.59%  
 Best Local Similarity: 92.59%  
 Query Match: 59.36%  
 DB: 4  
 Conservative: 0  
 Mismatches: 4  
 Indels: 6  
 Gaps: 1

US-09-674-266A-181 (1-206) x US-09-606-421B-282 (1-404)

QY 13 ProHisProSerArgLeuThrGlnGlyArgTyrValArgLysSerArgValAlaMet 32  
 DB 16 CCGCATCTTANNCGCGACTCACAAAGC-----AGAGTNGCCATG 57  
 QY 33 GluLysIleProValSerAlaPheLeuLeuLeuValAlaLeuSerTyrThrLeuAlaArg 52  
 DB 58 GAGAAATTCACAGTGTCCAGATTCTTGTCTCTTGTGGCCCTCTCTACACTCTGGCCAGA 117  
 QY 53 AspThrThrValLysProGlyAlaLysLysAspThrLysAspSerArgProLysLeuPro 72  
 DB 118 GATACCACAGTCAAACTGNAGCCAAAAGGACACAAAGGACTCTCGACCCAACTGCC 177  
 QY 73 GlnThrLeuSerArgGlyTyrGlyAspGlnLeuIleTyrThrGlnThrTyrGluAla 92  
 DB 178 CANACCTCTCCAGAGTTGGGGTGACCAACTCATCTGGACTCANACATATGAGAAGCT 237  
 QY 93 LeuTyrLysSerLysThrSerAsnLysProLeuMetIleIleHisLeuAspGluCys 112  
 DB 238 CTATATAAATCCAAGACAGCAACAAACCCCTTGATGATTATTCATCATTGGATGAGTGC 297  
 QY 113 ProHisSerGlnAlaLeuLysValPheAlaGluAsnLysGluIleGlnLysLeuAla 132  
 DB 298 CCACACAGTCAAGCTTTAAAGAAAGTGTGTGCTGAAAAATAAGAAAAATCCAGAAATTGGCA 357  
 QY 133 GluGlnPheValLeuLeuAsnLeuValTyrGluThrThrAspLys 147  
 DB 358 GAGCAGTTTGTCTCTCAATCTGGTTATGAAACAACCTGACANA 402

Search completed: November 30, 2003, 04:51:26  
 Job time : 67 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 26, 2003, 15:55:59 ; Search time 31 Seconds  
(without alignments)  
1225.655 Million cell updates/sec

Title: US-09-674-266a-181

Perfect score: 1063

Sequence: 1 RLSCAGTSLSGPHPSRLT.....DTALLDNMKKALKLKTTEL 206

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 18443283 residues

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

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3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
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10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
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13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
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17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1002	94.3	202	15	US-10-106-698-6395
2	899	84.6	175	10	US-09-792-439-2
3	899	84.6	175	12	US-10-237-496-28
4	899	84.6	175	12	US-10-242-074-28
5	899	84.6	175	12	US-10-242-505-28
6	899	84.6	175	12	US-10-242-574-28
7	899	84.6	175	12	US-10-243-261-28
8	899	84.6	175	12	US-10-243-282-28
9	899	84.6	175	12	US-10-243-402-28
10	899	84.6	175	12	US-10-243-431-28
11	899	84.6	175	12	US-10-245-164-28
12	899	84.6	175	12	US-09-903-190-106
13	899	84.6	175	12	US-10-244-972-28
14	899	84.6	175	12	US-10-197-942-28
15	899	84.6	175	12	US-10-238-196-28

16	899	84.6	175	12	US-10-245-013-28	Sequence 28, Appl
17	899	84.6	175	15	US-10-078-337-2	Sequence 2, Appl
18	899	84.6	175	15	US-10-245-103-28	Sequence 28, Appl
19	899	84.6	175	15	US-10-245-107-28	Sequence 28, Appl
20	899	84.6	175	15	US-10-245-143-28	Sequence 28, Appl
21	899	84.6	175	15	US-10-245-771-28	Sequence 28, Appl
22	899	84.6	175	15	US-10-245-851-28	Sequence 28, Appl
23	899	84.6	175	15	US-10-245-883-28	Sequence 28, Appl
24	899	84.6	175	15	US-10-237-535-28	Sequence 28, Appl
25	899	84.6	175	15	US-10-238-183-28	Sequence 28, Appl
26	899	84.6	175	15	US-10-238-283-28	Sequence 28, Appl
27	899	84.6	175	15	US-10-238-370-28	Sequence 28, Appl
28	899	84.6	175	15	US-10-245-055-28	Sequence 28, Appl
29	899	84.6	175	15	US-10-245-147-28	Sequence 28, Appl
30	899	84.6	175	15	US-10-245-730-28	Sequence 28, Appl
31	899	84.6	175	15	US-10-245-739-28	Sequence 28, Appl
32	899	84.6	175	15	US-10-246-210-28	Sequence 28, Appl
33	899	84.6	175	15	US-10-239-196-28	Sequence 28, Appl
34	899	84.6	175	15	US-10-243-024-28	Sequence 28, Appl
35	899	84.6	175	15	US-10-243-095-28	Sequence 28, Appl
36	899	84.6	175	15	US-10-245-621-28	Sequence 28, Appl
37	899	84.6	175	15	US-10-245-880-28	Sequence 28, Appl
38	899	84.6	175	15	US-10-245-033-28	Sequence 28, Appl
39	899	84.6	175	15	US-10-243-095-28	Sequence 28, Appl
40	899	84.6	175	15	US-10-245-185-28	Sequence 28, Appl
41	899	84.6	175	15	US-10-245-427-28	Sequence 28, Appl
42	899	84.6	175	15	US-10-245-473-28	Sequence 28, Appl
43	899	84.6	175	15	US-10-245-770-28	Sequence 28, Appl
44	899	84.6	175	15	US-10-245-877-28	Sequence 28, Appl
45	899	84.6	175	15	US-10-246-976-28	Sequence 28, Appl

#### ALIGNMENTS

##### RESULT 1

US-10-106-698-6395  
; Sequence 6395, Application US/10106698  
; Publication No. US20030109690A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides

; FILE REFERENCE: PA005P1

; CURRENT APPLICATION NUMBER: US/10/106,698

; CURRENT FILING DATE: 2002-03-27

; PRIOR APPLICATION NUMBER: PCT/US00/26524

; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: US 60/157,137

; PRIOR FILING DATE: 1999-09-29

; PRIOR APPLICATION NUMBER: US 60/163,280

; PRIOR FILING DATE: 1999-11-03

; NUMBER OF SEQ ID NOS: 8564

; SOFTWARE: PatentIn ver. 3.0

; SEQ ID NO 6395

; LENGTH: 202

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: MISC\_FEATURE

; LOCATION: (1)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: MISC\_FEATURE

; LOCATION: (7)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-10-106-698-6395

Query Match

Best Local Similarity 94.3%; Score 1002; DB 15; Length 202;

Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PHSRRLTQGRVWRKSRVAMEKIPVSAFLLLVALSYTLARDTTVKPGAKDKTDSRPKLP 72

Db 9 PHSRRLTQGRVWRKSRVAMEKIPVSAFLLLVALSYTLARDTTVKPGAKDKTDSRPKLP 68

QY 73 QTLRSGDQLIWTQYEEALYKSTSNKPLMIHHLDECPHSQALKKVFPAENKEIQKLA 132  
DB 69 QTLRSGDQLIWTQYEEALYKSTSNKPLMIHHLDECPHSQALKKVFPAENKEIQKLA 128  
QY 133 EQVLLNLVYETTDKHLSPDQGVPRIMFVDPSTLRADITGRYSNRLYAYEPADTALL 192  
DB 129 EQVLLNLVYETTDKHLSPDQGVPRIMFVDPSTLRADITGRYSNRLYAYEPADTALL 188  
QY 193 DNMKALKLLKTEL 206  
DB 189 DNMKALKLLKTEL 202

## RESULT 2

US-09-792-439-2  
; Sequence 2, Application US/09792439  
; Patent No. US20020111303A1  
; GENERAL INFORMATION:  
; APPLICANT: Boyd, Robert Simon  
; APPLICANT: Stamps, Alasdair Craig  
; APPLICANT: Terrett, Jonathan Alexander  
; APPLICANT: Tyson, Kerry Louise  
; TITLE OF INVENTION: Diagnostic and Therapeutic Methods  
; FILE REFERENCE: 2543-1-005N  
; CURRENT APPLICATION NUMBER: US/09/792,439  
; CURRENT FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: GB 0004576.5  
; PRIOR FILING DATE: 2000-02-25  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: human  
US-09-792-439-2

Query Match 84.6%; Score 899; DB 10; Length 175;  
Best Local Similarity 100.0%; Pred. No. 2.1e-92;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 MEKIPVSAPLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLRSGDQLIWTQYEE 60  
QY 92 ALYKSTSNKPLMIHHLDECPHSQALKKVFPAENKEIQKLAQFVLLNLVYETTDKHLSP 151  
DB 61 ALYKSTSNKPLMIHHLDECPHSQALKKVFPAENKEIQKLAQFVLLNLVYETTDKHLSP 120  
QY 152 DQGVPRIMFVDPSTLRADITGRYSNRLYAYEPADTALLDNMKALKLLKTEL 206  
DB 121 DQGVPRIMFVDPSTLRADITGRYSNRLYAYEPADTALLDNMKALKLLKTEL 175

## RESULT 3

US-10-237-496-28  
; Sequence 28, Application US/10237496  
; Publication No. US20030138896A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3630R1C19  
; CURRENT APPLICATION NUMBER: US/10/242,074  
; CURRENT FILING DATE: 2002-09-11  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114

FILE REFERENCE: P3630R1C14  
; CURRENT APPLICATION NUMBER: US/10/237,496  
; CURRENT FILING DATE: 2002-09-06  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; PRIOR FILING DATE: 1998-06-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 28  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-237-496-28

Query Match 84.6%; Score 899; DB 12; Length 175;  
Best Local Similarity 100.0%; Pred. No. 2.1e-92;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 MEKIPVSAPLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLRSGDQLIWTQYEE 60  
QY 92 ALYKSTSNKPLMIHHLDECPHSQALKKVFPAENKEIQKLAQFVLLNLVYETTDKHLSP 151  
DB 61 ALYKSTSNKPLMIHHLDECPHSQALKKVFPAENKEIQKLAQFVLLNLVYETTDKHLSP 120  
QY 152 DQGVPRIMFVDPSTLRADITGRYSNRLYAYEPADTALLDNMKALKLLKTEL 206  
DB 121 DQGVPRIMFVDPSTLRADITGRYSNRLYAYEPADTALLDNMKALKLLKTEL 175

## RESULT 4

US-10-242-074-28  
; Sequence 28, Application US/10242074  
; Publication No. US20030138897A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3630R1C19  
; CURRENT APPLICATION NUMBER: US/10/242,074  
; CURRENT FILING DATE: 2002-09-11  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 30, 2003, 03:27:12 ; Search time 308 Seconds  
(without alignments)  
2203.591 Million cell updates/sec

Title: US-09-674-266A-181

Perfect score: 1063

Sequence: 1 RLSCAGTUSGSGPHPSRLT.....DTALLDNMKALKLKTLEL 206

Scoring table:

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2190069 seqs, 1647345023 residues

Total number of hits satisfying chosen parameters: 4380138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters: -DEV=xlh  
-MODEL=frame+ p2n.model  
-Q=/cgn2\_1/usPTO spool1/US09674266/runat\_26112003\_152750\_15846/app\_query.fasta\_1.391  
-DB=PublishedApplications NA -QWMS=fastcap -SUFFIX=rnpb -MINMATCH=0.1  
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
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-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 17: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1025	96.4	920	12	US-10-237-496-27

2	1025	96.4	920	12	US-10-242-074-27	Sequence 27, Appl
3	1025	96.4	920	12	US-10-242-505-27	Sequence 27, Appl
4	1025	96.4	920	12	US-10-242-574-27	Sequence 27, Appl
5	1025	96.4	920	12	US-10-243-261-27	Sequence 27, Appl
6	1025	96.4	920	12	US-10-243-282-27	Sequence 27, Appl
7	1025	96.4	920	12	US-10-243-402-27	Sequence 27, Appl
8	1025	96.4	920	12	US-10-243-431-27	Sequence 27, Appl
9	1025	96.4	920	12	US-10-245-164-27	Sequence 27, Appl
10	1025	96.4	920	12	US-10-244-972-27	Sequence 27, Appl
11	1025	96.4	920	12	US-10-197-942-27	Sequence 27, Appl
12	1025	96.4	920	12	US-10-238-196-27	Sequence 27, Appl
13	1025	96.4	920	12	US-10-245-013-27	Sequence 27, Appl
14	1025	96.4	920	14	US-10-245-103-27	Sequence 27, Appl
15	1025	96.4	920	14	US-10-245-107-27	Sequence 27, Appl
16	1025	96.4	920	14	US-10-245-143-27	Sequence 27, Appl
17	1025	96.4	920	14	US-10-245-771-27	Sequence 27, Appl
18	1025	96.4	920	14	US-10-245-851-27	Sequence 27, Appl
19	1025	96.4	920	14	US-10-245-883-27	Sequence 27, Appl
20	1025	96.4	920	14	US-10-237-535-27	Sequence 27, Appl
21	1025	96.4	920	14	US-10-238-183-27	Sequence 27, Appl
22	1025	96.4	920	14	US-10-238-283-27	Sequence 27, Appl
23	1025	96.4	920	14	US-10-238-370-27	Sequence 27, Appl
24	1025	96.4	920	14	US-10-245-055-27	Sequence 27, Appl
25	1025	96.4	920	14	US-10-245-147-27	Sequence 27, Appl
26	1025	96.4	920	14	US-10-245-730-27	Sequence 27, Appl
27	1025	96.4	920	14	US-10-245-739-27	Sequence 27, Appl
28	1025	96.4	920	14	US-10-246-210-27	Sequence 27, Appl
29	1025	96.4	920	14	US-10-239-196-27	Sequence 27, Appl
30	1025	96.4	920	14	US-10-243-024-27	Sequence 27, Appl
31	1025	96.4	920	14	US-10-243-409-27	Sequence 27, Appl
32	1025	96.4	920	14	US-10-245-621-27	Sequence 27, Appl
33	1025	96.4	920	14	US-10-245-880-27	Sequence 27, Appl
34	1025	96.4	920	14	US-10-245-033-27	Sequence 27, Appl
35	1025	96.4	920	14	US-10-243-095-27	Sequence 27, Appl
36	1025	96.4	920	14	US-10-245-185-27	Sequence 27, Appl
37	1025	96.4	920	14	US-10-245-427-27	Sequence 27, Appl
38	1025	96.4	920	14	US-10-245-473-27	Sequence 27, Appl
39	1025	96.4	920	14	US-10-245-770-27	Sequence 27, Appl
40	1025	96.4	920	14	US-10-245-877-27	Sequence 27, Appl
41	1025	96.4	920	14	US-10-246-976-27	Sequence 27, Appl
42	1025	96.4	920	14	US-10-243-320-27	Sequence 27, Appl
43	1025	96.4	920	14	US-10-242-743-27	Sequence 27, Appl
44	1025	96.4	920	14	US-10-242-845-27	Sequence 27, Appl
45	1025	96.4	920	14	US-10-237-636-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1  
US-10-237-496-27  
; Sequence 27, Application US/10237496  
; Publication No. US20030138896A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3630R1C4  
; CURRENT APPLICATION NUMBER: US/10/237,496  
; CURRENT FILING DATE: 2002-09-06  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114

PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/063046  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/065027  
PRIOR FILING DATE: 1997-11-10  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/086478  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090689  
PRIOR FILING DATE: 1998-06-25  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 116  
SEQ ID NO 27  
LENGTH: 920  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-237-496-27

Alignment Scores:  
Pred. No.: 1,33e-130 Length: 920  
Score: 1025.00 Matches: 203  
Percent Similarity: 98.54% Conservative: 0  
Best Local Similarity: 98.54% Mismatches: 3  
Query Match: 96.43% Indels: 1  
DB: Gaps: 0

US-09-674-266A-181 (1-206) x US-10-237-496-27 (1-920)

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DB 56 AGACTCAGCTGTGTCGACACCTCAGAAAGCTT-GGACCGCATCTAGCCGCCGACTCACA 114  
QY 21 GlnGlyArgTrpValArgLysSerArgValAlaMetGluLysIleProValSerAlaPhe 40  
DB 115 CAAGGCAGGTTGGGTGAGGAATCCAGAGTTGCCATGAGAAATTCAGTGTCCAGCATTC 174  
QY 41 LeuLeuLeuValAlaLeuSerTyThrLeuAlaArgAspThrThrValLysProGlyAla 60  
DB 175 TTGCTCTTGTGGCCCTCTCTACACTCTGCCAGATACACAGTCAAACTTGAGCC 234  
QY 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGly 80  
DB 235 AAAAAGGACACAAAGGACTCTGACCCAAACTGCCAGACCCCTCTCCAGAGTTGGGT 294  
QY 81 AspGlnLeuIleTrpThrGlnThrTyThrGluAlaLeuTyLysSerLysThrSerAsn 100  
DB 295 GACCAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAATCCAAAGCAAGCAAC 354  
QY 101 LysProLeuMetIleLeuHisLeuAspGluCysProHisSerGlnAlaLeuLysLys 120  
DB 355 AAACCTTGTATGATTATTCATCTAGTGGATGAGTGCACACAGTCAAGCTTTAAGAAA 414  
QY 121 ValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluGlnPheValLeuLeuAsnLeu 140  
DB 415 GTGTTTGTCTCAAAATAAAGAAATCCAGAAATTCGACAGCAGTTTGTCTCTCTCAATCTG 474  
QY 141 ValTyThrThrThrAspLysHisLeuSerProAspGlyGlnTyThrValProArgIleMet 160  
DB 475 GTTATGAAACAACTGACAAACACCTTTCTCTGATGGCCAGTATGTCCCGAGATTATG 534  
QY 161 PheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyThrSerAsnArgLeu 180  
DB 535 TTTGTTGACCCCACTCTGACAGTTAGAGCCGATATCATCTGAAGATATTCAATTCGTCTC 594  
QY 181 TyrAlaTyThrProAlaAspThrAlaLeuLeuLeuAspAsnMetLysLysAlaLeuLys 200

DB 595 TATGCTTACGAACCTGCAGATACAGCTCTGTTGTTGACACACATGAAGAAAGCTCTCAAG 654  
QY 201 LeuLeuLysThrGluLeu 206  
DB 655 TTGCTGAGAGACTGAATTG 672

RESULT 2  
US-10-242-074-27  
Sequence 27, Application US/10242074  
Publication No. US20030138897A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin  
APPLICANT: Eaton, Dan  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Phillippe  
APPLICANT: Watanabe, Colin  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
APPLICANT: Fong, Sherman  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3630R1C19  
CURRENT APPLICATION NUMBER: US/10/242,074  
CURRENT FILING DATE: 2002-09-11  
PRIOR APPLICATION NUMBER: 10/197942  
PRIOR FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 60/059114  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/063046  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/065027  
PRIOR FILING DATE: 1997-11-10  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/086478  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090689  
PRIOR FILING DATE: 1998-06-25  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 116  
SEQ ID NO 27  
LENGTH: 920  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-242-074-27

Alignment Scores:  
Pred. No.: 1,33e-130 Length: 920  
Score: 1025.00 Matches: 203  
Percent Similarity: 98.54% Conservative: 0  
Best Local Similarity: 98.54% Mismatches: 3  
Query Match: 96.43% Indels: 1  
DB: Gaps: 0

US-09-674-266A-181 (1-206) x US-10-242-074-27 (1-920)

QY 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgArgLeuThr 20  
DB 56 AGACTCAGCTGTGTCGACACCTCAGAAAGCTT-GGACCGCATCTAGCCGCCGACTCACA 114  
QY 21 GlnGlyArgTrpValArgLysSerArgValAlaMetGluLysIleProValSerAlaPhe 40  
DB 115 CAAGGCAGGTTGGGTGAGGAATCCAGAGTTGCCATGAGAAATTCAGTGTCCAGCATTC 174

QY 41 LeuLeuLeuValAlaLeuSerThrThrLeuAlaArgAspThrThrValLysProGlyAla 60  
DB 175 TTGCTCTTGTGGCTCTCTCTACACTCTGGCCAGAGATACACAGTCAAACTGGAGCC 234  
QY 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGly 80  
DB 235 AAAAGGACACAAAGACTCTCGACCCAACTGCCAGACCTCTCCAGAGTTGGGGT 294  
QY 81 AspGlnLeuLeuLeuThrThrGlnThrThrGluGluAlaLeuThrLysSerLysThrSerAsn 100  
DB 295 GACCAACTCATCTGACTCAGACATATGAGAGCTCTATATAATCCAGACAGCAAC 354  
QY 101 LysProLeuMetIleIleHisLeuAspGluCysProHisSerGlnAlaLeuLysLys 120  
DB 355 AAACCTTGTGATGATTATTCATCATCTGGATGAGTGGCCACACAGTCAAGCTTTAAAGAA 414  
QY 121 ValPheAlaGluAsnLysGluLeuGlnLysLeuAlaGluGlnPheValLeuLeuAsnLeu 140  
DB 415 GTGTTTGTCTGAAATAAAGAAATCCAGAAATTTGGCAGAGCAGTTTGTCTCTCAATCTG 474  
QY 141 ValTyGluThrThrAspLysHisLeuSerProAspGlyGlnThrValProArgIleMet 160  
DB 475 GTTTATGAACAACCTGACAAACCTTCTCTGATGGCCAGTATGTCCCCAGGATTATG 534  
QY 161 PheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTy+SerAsnArgLeu 180  
DB 535 TTTGTTGACCCATCTCTGACAGTGTAGGCCGATATCACTGGAAGATATTTCAATCGTCTC 594  
QY 181 TyrAlaTyGluProAlaAspThrAlaLeuLeuAspAsnMetLysLysAlaLeuLys 200  
DB 595 TATGCTTACGAACCTCGCATACAGCTCTGTTGTTGATGAAACATGAAGAAAGCTCTCAAG 654  
QY 201 LeuLeuLysThrGluLeu 206  
DB 655 TTGCTGAAGACTGAATTG 672

## RESULT 3

US-10-242-505-27  
; Sequence 27, Application US/10242505  
; Publication No. US2003013898A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3630R1C25  
; CURRENT APPLICATION NUMBER: US/10/242, 505  
; CURRENT FILING DATE: 2002-09-11  
; PRIORITY APPLICATION NUMBER: 10/197942  
; PRIORITY FILING DATE: 2002-07-18  
; PRIORITY APPLICATION NUMBER: 60/059114  
; PRIORITY FILING DATE: 1997-09-17  
; PRIORITY APPLICATION NUMBER: 60/063046  
; PRIORITY FILING DATE: 1997-10-24  
; PRIORITY APPLICATION NUMBER: 60/065027  
; PRIORITY FILING DATE: 1997-11-10  
; PRIORITY APPLICATION NUMBER: 60/079689  
; PRIORITY FILING DATE: 1998-03-27  
; PRIORITY APPLICATION NUMBER: 60/086478  
; PRIORITY FILING DATE: 1998-05-22  
; PRIORITY APPLICATION NUMBER: 60/087607  
; PRIORITY FILING DATE: 1998-06-02

; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; PRIOR FILING DATE: 1998-06-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 27  
; LENGTH: 920  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-242-505-27  
Alignment Scores:  
Pred. No.: 1,33e-130 Length: 920  
Score: 1025.00 Matches: 203  
Percent Similarity: 98.54% Conservative: 0  
Best Local Similarity: 98.54% Mismatches: 3  
Query Match: 96.43% Indels: 1  
DB: 12 Gaps: 0

US-09-674-266A-181 (1-206) x US-10-242-505-27 (1-920)

QY 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgArgLeuThr 20  
DB 56 AGACTCAGCTGTGCTGGCAGACTCAGAAAGCTT-GGACCGCATCTTAGCGCGGACTCACA 114  
QY 21 GlnGlyArgTrpValArgLysSerArgValAlaMetGluLysIleProValSerIlePhe 40  
DB 115 CAAGCAGGTGGGTGAGGAAATCCAGAGTTCGCCATGGAGAAATTTCCAGTGTGACATTC 174  
QY 41 LeuLeuLeuValAlaLeuSerThrThrLeuAlaArgAspThrThrValLysProGlyAla 60  
DB 175 TTGCTCTTGTGGCCCTCTCTACACTCTGCCAGAGATACACAGTCAACCTGGAGCC 234  
QY 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGly 80  
DB 235 AAAAGGACACAAAGACTCTCGACCCAACTGCCAGACCTCTCCAGAGTTGGGGT 294  
QY 81 AspGlnLeuLeuLeuThrThrGlnThrThrGluGluAlaLeuThrLysSerLysThrSerAsn 100  
DB 295 GACCAACTCATCTGACTCAGACATATGAAGAAGCTCTATATAATCCAGACAGCAAC 354  
QY 101 LysProLeuMetIleIleHisLeuAspGluCysProHisSerGlnAlaLeuLysLys 120  
DB 355 AAACCTTGTGATGATTATTCATCATCTGGATGAGTGGCCAGTATGTCCCCAGGATTATG 414  
QY 121 ValPheAlaGluAsnLysGluLeuGlnLysLeuAlaGluGlnPheValLeuLeuAsnLeu 140  
DB 415 GTGTTTGTCTGAAATAAAGAAATCCAGAAATTTGGCAGAGCAGTTTGTCTCTCAATCTG 474  
QY 141 ValTyGluThrThrAspLysHisLeuSerProAspGlyGlnThrValProArgIleMet 160  
DB 475 GTTTATGAACAACCTGACAAACCTTCTCTGATGGCCAGTATGTCCCCAGGATTATG 534  
QY 161 PheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTy+SerAsnArgLeu 180  
DB 535 TTTGTTGACCCATCTCTGACAGTGTAGGCCGATATCACTGGAAGATATTTCAATCGTCTC 594  
QY 181 TyrAlaTyGluProAlaAspThrAlaLeuLeuAspAsnMetLysLysAlaLeuLys 200  
DB 595 TATGCTTACGAACCTCGCATACAGCTCTGTTGTTGATGAAACATGAAGAAAGCTCTCAAG 654  
QY 201 LeuLeuLysThrGluLeu 206  
DB 655 TTGCTGAAGACTGAATTG 672

## RESULT 4

US-10-242-574-27  
; Sequence 27, Application US/10242574  
; Publication No. US2003013899A1  
; GENERAL INFORMATION:





ORGANISM: Homo Sapien  
US-10-243-261-27

Alignment Scores:  
Pred. No.: 1,33e-130 Length: 920  
Score: 1025.00 Matches: 203  
Percent Similarity: 98.54% Conservative: 0  
Best Local Similarity: 98.54% Mismatches: 3  
Query Match: 96.43% Indels: 1  
DB: 12 Gaps: 0

US-09-674-266A-181 (1-206) x US-10-243-261-27 (1-920)

```
QY 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgLeuThr 20
   |||||
Db 56 AGACTCAGCTGTGCTGGCACACTCAGAAGCTT-GGACCGCATCTTAGCGCGGACTCACA 114

QY 21 GlnGlyArgTTPValArgLysSerArgValAlaMetGluLysIleProValSerAlaPhe 40
   |||||
Db 115 CAAGCAGGTGGGTGAGGAAATCCAGAGTTGCCATGGAGAAATTCAGTGTTCAGCATTC 174

QY 41 LeuLeuValAlaLeuSerTyrThrLeuAlaArgAspThrThrValLysProGlyAla 60
   |||||
Db 175 TTGCTCTTGTGGCCCTCTCTACACTCTGGCCAGAGATACCACAGTCAAACTTGAGCC 234

QY 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTTPGly 80
   |||||
Db 235 AAAAAGGACACAAAGGACTCTCGACCCAAACTGCCAGACCTCTCCAGAGGTTGGGT 294

QY 81 AspGlnLeuIleTTPThrGlnThrTyrGluGluAlaLeuTyrLysSerLysThrSerAsn 100
   |||||
Db 295 GACCAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAAATCCAAAGCAAGCAAC 354

QY 101 LysProLeuMetIleLeuHisLeuAspGluCysProHisSerGlnAlaLeuLysLys 120
   |||||
Db 355 AAACCTTGATGATTATTCATCAGTGTGGAGTGGCCACAGTCAAGCTTTAAAGAAA 414

QY 121 ValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluGlnPheValLeuAsnLeu 140
   |||||
Db 415 GTGTTTGTGCTGAAATTAAGAAATCCAGAAATTTGGCAGAGCAGTCTCTCTCAATCTG 474

QY 141 ValTyrGluThrThrAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMet 160
   |||||
Db 475 GTTTATGAACAACTCACAACACCTTTCTCTGATGGCCAGTATGTCCTCCAGGATTATG 534

QY 161 PheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnArgLeu 180
   |||||
Db 535 TTGTGTGACCAATCTCTGACAGTTAGAGCCGATATACATGGAAGATATTCAAATCGTCTC 594

QY 181 TyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLysLysAlaLeuLys 200
   |||||
Db 595 TATGCTTACGAACCTGCAGATACAGCTCTGTGTTGCTTGACACATGAGAAAGCTCTCAAG 654

QY 201 LeuLeuLysThrGluLeu 206
   |||||
Db 655 TTGCTGAAGACTGAATTG 672
```

## RESULT 6

US-10-243-282-27  
; Sequence 27, Application US/10243282  
; Publication No. US20030138901A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin

APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3630R1C50  
; CURRENT APPLICATION NUMBER: US/10/243,282  
; CURRENT FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; PRIOR FILING DATE: 1998-06-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 27  
; LENGTH: 920  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-243-282-27

Alignment Scores:  
Pred. No.: 1,33e-130 Length: 920  
Score: 1025.00 Matches: 203  
Percent Similarity: 98.54% Conservative: 0  
Best Local Similarity: 98.54% Mismatches: 3  
Query Match: 96.43% Indels: 1  
DB: 12 Gaps: 0

US-09-674-266A-181 (1-206) x US-10-243-282-27 (1-920)

```
QY 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgLeuThr 20
   |||||
Db 56 AGACTCAGCTGTGCTGGCACACTCAGAAGCTT-GGACCGCATCTTAGCGCGGACTCACA 114

QY 21 GlnGlyArgTTPValArgLysSerArgValAlaMetGluLysIleProValSerAlaPhe 40
   |||||
Db 115 CAAGCAGGTGGGTGAGGAAATCCAGAGTTGCCATGGAGAAATTCAGTGTTCAGCATTC 174

QY 41 LeuLeuValAlaLeuSerTyrThrLeuAlaArgAspThrThrValLysProGlyAla 60
   |||||
Db 175 TTGCTCTTGTGGCCCTCTCTACACTCTGGCCAGAGATACCACAGTCAAACTTGAGCC 234

QY 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTTPGly 80
   |||||
Db 235 AAAAAGGACACAAAGGACTCTCGACCCAAACTGCCAGACCTCTCCAGAGGTTGGGT 294

QY 81 AspGlnLeuIleTTPThrGlnThrTyrGluGluAlaLeuTyrLysSerLysThrSerAsn 100
   |||||
Db 295 GACCAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAAATCCAAAGCAAGCAAC 354

QY 101 LysProLeuMetIleLeuHisLeuAspGluCysProHisSerGlnAlaLeuLysLys 120
   |||||
Db 355 AAACCTTGATGATTATTCATCAGTGTGGAGTGGCCACAGTCAAGCTTTAAAGAAA 414

QY 121 ValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluGlnPheValLeuAsnLeu 140
   |||||
Db 415 GTGTTTGTGCTGAAATTAAGAAATTCAGAAATTTGGCAGAGCAGTCTCTCTCAATCTG 474

QY 141 ValTyrGluThrThrAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMet 160
   |||||
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; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 27
; LENGTH: 920
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-243-431-27

Alignment Scores:
Pred. No.: 1,33e-130 Length: 920
Score: 1025.00 Matches: 203
Percent Similarity: 98.54% Conservative: 0
Best Local Similarity: 98.54% Mismatches: 3
Query Match: 96.43% Indels: 1
DB: 12 Gaps: 0

US-09-674-266A-181 (1-206) x US-10-243-431-27 (1-920)

QY 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgArgLeuThr 20
DB 56 AGACTCAGCTGTGCTGGACACTCAGAGCTT-GGACCGCATCTTAGCGCGGACTCACA 114

QY 21 GlnGlyArgTTPValArgLysSerArgValAlaMetGluLysIleProValSerAlaPhe 40
DB 115 CAAGGCAGGTGGTGGAGAAATCCAGAGTTGCCATGGAGAAATTCAGTGTCCAGCATTC 174

QY 41 LeuLeuLeuValAlaLeuSerTyrThrLeuAlaArgAspThrThrValLysProGlyAla 60
DB 175 TTGCTCCTGTGGCCCTCTCTACACTCTGGCCAGAGATACACAGTCAAACTCGAGCC 234

QY 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTTPGly 80
DB 235 AAAAGGACAAAGAGCTCTCGACCCAACTGCCCGCCAGCCCTCTCAGAGGTGGGT 294

QY 81 AspGlnLeuIleTTPThrGlnThrTyrGluGluAlaLeuTyrLysSerLysThrSerAsn 100
DB 295 GACCAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAATCCAAGACAGCAAC 354

QY 101 LysProLeuMetIleIleHisHisLeuAspGluCysProHisSerGlnAlaLeuLysLys 120
DB 355 AAACCCCTTGATGATTATTCATCACTTGGATGAGTCCACACAGTCAAGCTTTAAAGAAA 414

QY 121 ValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluInPheValLeuAsnLeu 140
DB 415 GGTGTTGCTGAAATTAAGAAATCCAGAAATGGCAGAGCAGTTGTCTCTCTCAATCTG 474

QY 141 ValTyrGluThrThrAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMet 160
DB 475 GTTTATGAACAACATGACAAACACTTCTCTGTATGGCCAGTATGTCACGAGTTATG 534

QY 161 PheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnArgLeu 180
DB 535 TTTGTTGACCCATCTCTGACAGTTCAGAGCCGATATCACTGGAAGATATTTCAATCGTCTC 594

QY 181 TyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLysLysAlaLeuLys 200
DB 595 TATGCTTACGAACCTGCGAGATACAGCTCTGTGTGCTTGACAAATCAATGAAGAAAGCTCTCAAG 654

QY 201 LeuLeuLysThrGluLeu 206
DB 655 TTGCTGAAGACTGAATTG 672

RESULT 9
US-10-245-164-27
; Sequence 27, Application US/10245164
; Publication No. US20030138904A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C76
; CURRENT APPLICATION NUMBER: US/10/245,164
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 27
; LENGTH: 920
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-245-164-27

Alignment Scores:
Pred. No.: 1,33e-130 Length: 920
Score: 1025.00 Matches: 203
Percent Similarity: 98.54% Conservative: 0
Best Local Similarity: 98.54% Mismatches: 3
Query Match: 96.43% Indels: 1
DB: 12 Gaps: 0

US-09-674-266A-181 (1-206) x US-10-245-164-27 (1-920)

QY 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgArgLeuThr 20
DB 56 AGACTCAGCTGTGCTGGACACTCAGAGCTT-GGACCGCATCTTAGCGCGGACTCACA 114

QY 21 GlnGlyArgTTPValArgLysSerArgValAlaMetGluLysIleProValSerAlaPhe 40
DB 115 CAAGGCAGGTGGTGGAGAAATCCAGAGTTGCCATGGAGAAATTCAGTGTCCAGCATTC 174

QY 41 LeuLeuLeuValAlaLeuSerTyrThrLeuAlaArgAspThrThrValLysProGlyAla 60
DB 175 TTGCTCCTGTGGCCCTCTCTACACTCTGGCCAGAGATACACAGTCAAACTCGAGCC 234

QY 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTTPGly 80
DB 235 AAAAGGACAAAGAGCTCTCGACCCAACTGCCCGCCAGCCCTCTCAGAGGTGGGT 294

QY 81 AspGlnLeuIleTTPThrGlnThrTyrGluGluAlaLeuTyrLysSerLysThrSerAsn 100
DB 295 GACCAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAATCCAAGACAGCAAC 354

QY 101 LysProLeuMetIleIleHisHisLeuAspGluCysProHisSerGlnAlaLeuLysLys 120
DB 355 AAACCCCTTGATGATTATTCATCACTTGGATGAGTCCACACAGTCAAGCTTTAAAGAAA 414

QY 121 ValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluInPheValLeuAsnLeu 140
DB 415 GGTGTTGCTGAAATTAAGAAATCCAGAAATGGCAGAGCAGTTGTCTCTCTCAATCTG 474

QY 141 ValTyrGluThrThrAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMet 160
DB 475 GTTTATGAACAACATGACAAACACTTCTCTGTATGGCCAGTATGTCACGAGTTATG 534

QY 161 PheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnArgLeu 180
DB 535 TTTGTTGACCCATCTCTGACAGTTCAGAGCCGATATCACTGGAAGATATTTCAATCGTCTC 594

QY 181 TyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLysLysAlaLeuLys 200
DB 595 TATGCTTACGAACCTGCGAGATACAGCTCTGTGTGCTTGACAAATCAATGAAGAAAGCTCTCAAG 654
```

```
Db 175 TTGCTCTTGGCCCTCTCTACACTCTGGCAGAGATACCAAGTCAACCTGGAGCC 234
Qy 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGly 80
Db 235 AAAAAGGACAAAGGACTCTCGACCCCAAACTGCCAGACCCCTCTCCAGAGGTGGGGT 294
Qy 81 AspGlnLeuLeuTrpThrGlnThrTyrGluGluAlaLeuTyrLysSerLysThrSerAsn 100
Db 295 GACCAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAATCCAAGACAAGCAAC 354
Qy 101 LysProLeuMetIleIleHisLeuAspGluCysProHisSerGlnAlaLeuLysLys 120
Db 355 AAACCCCTTGATGATTATTCATCACTTCGATGAGTGGCCACACAGTCAAGCTTTAAAGAA 414
Qy 121 ValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluGlnPheValLeuLeuAsnLeu 140
Db 415 GTGTTTGTCTGAAAATAAAGAAATCCAGAAATTCGACAGCAGTTTGTCTCTCAATCTG 474
Qy 141 ValTyrGluThrThrAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMet 160
Db 475 GTTTATGAACAACCTGACAAACACCTTCTCTGATGGCCAGATATGCCCCAGGATTATG 534
Qy 161 PheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnArgLeu 180
Db 535 TTGTTGACCCATCTCTGACAGTTAGAGCCGATATCACTGGAGATATTCAAATCGTCTC 594
Qy 181 TyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLysLysAlaLeuLys 200
Db 595 TATGCTTACGAACCTGCAGATACAGCTCTGTGCTTGACAAACATGAAGAAAGCTCTCAAG 654
Qy 201 LeuLeuLysThrGluLeu 206
Db 655 TTGCTGAAGACTGAATTG 672
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## RESULT 10

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US-10-244-972-27
; Sequence 27, Application US/10244972
; Publication No. US20030170809A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C75
; CURRENT APPLICATION NUMBER: US/10/244,972
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
```

```
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 27
; LENGTH: 920
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-244-972-27

Alignment Scores:
Pred. No.: 1,33e-130 Length: 920
Score: 1025.00 Matches: 203
Percent Similarity: 98.54% Conservative: 0
Best Local Similarity: 98.54% Mismatches: 3
Query Match: 96.43% Indels: 1
DB: 12 Gaps: 0

US-09-674-266A-181 (1-206) x US-10-244-972-27 (1-920)
Qy 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgArgLeuThr 20
Db 56 AGACTCAGCTGTGCTGGCACACTCAGAAGCTT-GGACCGCATCTTAGCCGCCGACTCACA 114
Qy 21 GlnGlyArgTrpValArgLysSerArgValAlaMetGluLysIleProValSerAlaPhe 40
Db 115 CAAGCAGGCTGGGTGAGGAAATCCAGAGTTGCCATGGAGAAATTCAGGTGCAGCATTC 174
Qy 41 LeuLeuLeuValAlaLeuSerTyrThrLeuAlaArgAspThrThrValLysProGlyAla 60
Db 175 TTGCTCTTGTGGCCCTCTCTACACTCTGGCCAGAGATACCAAGTCAACCTCGAGCC 234
Qy 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGly 80
Db 235 AAAAAGGACAAAGGACTCTCGACCCAAACTGCCCCAGACCCCTCTCCAGAGGTGGGGT 294
Qy 81 AspGlnLeuLeuTrpThrGlnThrTyrGluGluAlaLeuTyrLysSerLysThrSerAsn 100
Db 295 GACCAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAATCCAAGACAAGCAAC 354
Qy 101 LysProLeuMetIleIleHisLeuAspGluCysProHisSerGlnAlaLeuLysLys 120
Db 355 AAACCCCTTGATGATTATTCATCACTTGGATGAGTGGCCACACAGTCAAGCTTTAAAGAA 414
Qy 121 ValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluGlnPheValLeuLeuAsnLeu 140
Db 415 GTGTTTGTCTGAAAATAAAGAAATCCAGAAATTCGACAGCAGTTTGTCTCTCAATCTG 474
Qy 141 ValTyrGluThrThrAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMet 160
Db 475 GTTTATGAACAACCTGACAAACACCTTCTCTGATGGCCAGATATGCCCCAGGATTATG 534
Qy 161 PheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnArgLeu 180
Db 535 TTGTTGACCCATCTCTGACAGTTAGAGCCGATATCACTGGAAGATATTCAAATCGTCTC 594
Qy 181 TyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLysLysAlaLeuLys 200
Db 595 TATGCTTACGAACCTGCAGATACAGCTCTGTGCTTGACAAACATGAAGAAAGCTCTCAAG 654
Qy 201 LeuLeuLysThrGluLeu 206
Db 655 TTGCTGAAGACTGAATTG 672

RESULT 11
US-10-197-942-27
; Sequence 27, Application US/10197942
; Publication No. US20030175882A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
```

APPLICANT: Filvaroff, Ellen  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe  
APPLICANT: Watanabe, Colin  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
APPLICANT: Fong, Sherman  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3630R1C1(US)  
CURRENT APPLICATION NUMBER: US/10/197,942  
CURRENT FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 60/059114  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/063046  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/065027  
PRIOR FILING DATE: 1997-11-10  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/086478  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090689  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/091358  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/099803  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/106932  
PRIOR FILING DATE: 1998-11-03  
PRIOR APPLICATION NUMBER: 60/115554  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/119342  
PRIOR FILING DATE: 1999-02-09  
PRIOR APPLICATION NUMBER: 60/123957  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123972  
PRIOR FILING DATE: 1999-03-11  
PRIOR APPLICATION NUMBER: 60/127372  
PRIOR FILING DATE: 1999-04-01  
PRIOR APPLICATION NUMBER: 60/131271  
PRIOR FILING DATE: 1999-04-27  
PRIOR APPLICATION NUMBER: 60/133459  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 60/135725  
PRIOR FILING DATE: 1999-05-25  
PRIOR APPLICATION NUMBER: 60/135729  
PRIOR FILING DATE: 1999-05-25  
PRIOR APPLICATION NUMBER: 60/135750  
PRIOR FILING DATE: 1999-05-25  
PRIOR APPLICATION NUMBER: 60/138385  
PRIOR FILING DATE: 1999-06-09  
PRIOR APPLICATION NUMBER: 60/140653  
PRIOR FILING DATE: 1999-06-22  
PRIOR APPLICATION NUMBER: 60/141037  
PRIOR FILING DATE: 1999-06-23  
PRIOR APPLICATION NUMBER: 60/144732  
PRIOR FILING DATE: 1999-07-20  
PRIOR APPLICATION NUMBER: 60/144758  
PRIOR FILING DATE: 1999-07-20  
PRIOR APPLICATION NUMBER: 60/144790  
PRIOR FILING DATE: 1999-07-20  
PRIOR APPLICATION NUMBER: 60/145228  
PRIOR FILING DATE: 1999-07-20  
PRIOR APPLICATION NUMBER: 60/145698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: 60/146222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: 60/146843  
PRIOR FILING DATE: 1999-08-03  
PRIOR APPLICATION NUMBER: 60/148188  
PRIOR FILING DATE: 1999-08-10  
PRIOR APPLICATION NUMBER: 60/148513  
PRIOR FILING DATE: 1999-08-12  
PRIOR APPLICATION NUMBER: 60/149327  
PRIOR FILING DATE: 1999-08-17  
PRIOR APPLICATION NUMBER: 60/149395  
PRIOR FILING DATE: 1999-08-17  
PRIOR APPLICATION NUMBER: 60/150114  
PRIOR FILING DATE: 1999-08-20  
PRIOR APPLICATION NUMBER: 60/151700  
PRIOR FILING DATE: 1999-08-31  
PRIOR APPLICATION NUMBER: 60/151734  
PRIOR FILING DATE: 1999-08-31  
PRIOR APPLICATION NUMBER: 60/162506  
PRIOR FILING DATE: 1999-10-29  
PRIOR APPLICATION NUMBER: 60/170262  
PRIOR FILING DATE: 1999-12-09  
PRIOR APPLICATION NUMBER: 60/177118  
PRIOR FILING DATE: 2000-01-20  
PRIOR APPLICATION NUMBER: 60/179851  
PRIOR FILING DATE: 2000-02-02  
PRIOR APPLICATION NUMBER: 60/180921  
PRIOR FILING DATE: 2000-02-08  
PRIOR APPLICATION NUMBER: 60/187202  
PRIOR FILING DATE: 2000-03-03  
PRIOR APPLICATION NUMBER: 60/198587  
PRIOR FILING DATE: 2000-04-18  
PRIOR APPLICATION NUMBER: 60/199614  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: 60/206330  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/206368  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/209832  
PRIOR FILING DATE: 2000-06-05  
PRIOR APPLICATION NUMBER: 60/218371  
PRIOR FILING DATE: 2000-07-13  
PRIOR APPLICATION NUMBER: 60/222695  
PRIOR FILING DATE: 2000-08-02  
PRIOR APPLICATION NUMBER: 60/229896  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/230621  
PRIOR FILING DATE: 2000-09-05  
PRIOR APPLICATION NUMBER: 60/232887  
PRIOR FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: 60/235147  
PRIOR FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: 60/261878  
PRIOR FILING DATE: 2001-01-12  
PRIOR APPLICATION NUMBER: 60/261910  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: 60/261939  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: 60/262150  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: 60/264395  
PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: 60/266421  
PRIOR FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: 60/267623  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/274399  
PRIOR FILING DATE: 2001-03-09  
PRIOR APPLICATION NUMBER: 60/280982

PRIOR FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: 60/282129  
PRIOR FILING DATE: 2001-04-04  
PRIOR APPLICATION NUMBER: 60/282199  
PRIOR FILING DATE: 2001-04-04  
PRIOR APPLICATION NUMBER: 60/290589  
PRIOR FILING DATE: 2001-05-09  
PRIOR APPLICATION NUMBER: 09/180997  
PRIOR FILING DATE: 1998-11-19  
PRIOR APPLICATION NUMBER: 09/267213  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 09/380137  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 09/380138  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 09/403297  
PRIOR FILING DATE: 1999-10-18  
PRIOR APPLICATION NUMBER: 09/423741  
PRIOR FILING DATE: 1999-11-10  
PRIOR APPLICATION NUMBER: 09/709238  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 09/802706  
PRIOR FILING DATE: 2001-03-09  
PRIOR APPLICATION NUMBER: 09/872035  
PRIOR FILING DATE: 2001-06-01  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 09/924419  
PRIOR FILING DATE: 2001-08-06  
PRIOR APPLICATION NUMBER: 09/927796  
PRIOR FILING DATE: 2001-08-09  
PRIOR APPLICATION NUMBER: 09/929404  
PRIOR FILING DATE: 2001-08-13  
PRIOR APPLICATION NUMBER: 09/931836  
PRIOR FILING DATE: 2001-08-16  
PRIOR APPLICATION NUMBER: 09/941992  
PRIOR FILING DATE: 2001-08-28  
PRIOR APPLICATION NUMBER: 09/946374  
PRIOR FILING DATE: 2001-09-04  
PRIOR APPLICATION NUMBER: 10/001054  
PRIOR FILING DATE: 2001-11-30  
PRIOR APPLICATION NUMBER: 10/052586  
PRIOR FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: 10/081056  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: 10/119480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: PCT/US98/18824  
PRIOR FILING DATE: 1998-09-10

Alignment Scores:  
Pred. No.: 1.33e-130 Length: 920  
Score: 1025.00 Matches: 203  
Percent Similarity: 98.54% Conservative: 0  
Best Local Similarity: 98.54% Mismatches: 3  
Query Match: 96.43% Indels: 1  
DB: 12 Gaps: 0

US-09-674-266A-181 (1-206) x US-10-197-942-27 (1-920)

Qy 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgArgLeuThr 20  
Db 56 AGACTCAGCTGTGTCGACACTCAGAGCTT-GGACCGCATCTCCGCCGCACTCACA 114  
Qy 21 GlnGlyArgTrpValArgLysSerArgValAlaMetGluLysIleProValSerAlaPhe 40  
Db 115 CAAGCCAGGTGGGTGACGAAATCCAGATGGCCATGAGAAATTCAGTGTGAGCATTC 174  
Qy 41 LeuLeuValAlaLeuSerTyThrLeuAlaArgAspThrThrValLysProGlyAla 60  
Db 175 TTGCTCCTTGGCCCTCTCTACACTCTGCCAGATACACAGTCAAACTGGAGCC 234  
Qy 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGly 80

Db 235 AAAAGGACACAAAGGACTCTCGACCCAAACTGCCCCAGACCTCTCCAGAGGTGGGGT 294  
Qy 81 AspGlnLeuIleTrpThrGlnThrTyThrGluGluAlaLeuTyLysSerLysThrSerAsn 100  
Db 295 GACCAACTCATCTGGACTCAGACATATGAAGAAGCTCTATATAATCCAAAGCAAC 354  
Qy 101 LysProLeuMetIleIleHisHisLeuAspGluCysProHisSerGlnAlaLeuLysLys 120  
Db 355 AAACCTTGTATGATTAATTCATCTTGGATGAGTGGCCACACAGTCAAGCTTTAAAGAA 414  
Qy 121 ValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluGlnPheValLeuLeuAsnLeu 140  
Db 415 GTGTTTGTCTGAAATAAAGAAATCCAGAAATTCGAGAGCAGTTTGTCTCTCTCAATCTG 474  
Qy 141 ValTyGluThrThrAspLysHisLeuSerProAspGlyGlnTyThrValProArgIleMet 160  
Db 475 GTTTATGAAACAACTGACAAACACCTTTCTCTGTATGGCCAGTATGTCCCAGGATTATG 534  
Qy 161 PheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyThrSerAsnArgLeu 180  
Db 535 TTTGTTGACCATCTCTGACAGTTAGCCGATATCACTGGAAGATATTCAAATCGTCTC 594  
Qy 181 TyrAlaTyGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLysLysAlaLeuLys 200  
Db 595 TATGCTTACGAACCTGCAGATACAGCTCTGTCTGTTGACAAACATGAAGAAGCTCTCAAG 654  
Qy 201 LeuLeuLysThrGluLeu 206  
Db 655 TTGCTGAAGACTGAATTG 672

RESULT 12  
US-10-238-196-27  
; Sequence 27, Application US/10238196  
; Publication No. US20030186372A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Baton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3630R1C8  
; CURRENT APPLICATION NUMBER: US/10/238,196  
; CURRENT FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; PRIOR FILING DATE: 1998-06-25

; Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 116

; SEQ ID NO 27

; LENGTH: 920

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-238-196-27

Alignment Scores:

Pred. No.: 1.33e-130 Length: 920  
Score: 1025.00 Matches: 203  
Percent Similarity: 98.54% Conservatives: 0  
Best Local Similarity: 98.54% Mismatches: 3  
Query Match: 96.43% Indels: 1  
DB: 12 Gaps: 0

US-09-674-266A-181 (1-206) x US-10-238-196-27 (1-920)

QY 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgLeuThr 20  
DB 56 AGACTCAGCTGTGCTGGCACACTCAGAAGCTT-GGACCGCATCTAGCCGCGACTCACA 114  
QY 21 GlnGlyArgTrpValArgLysSerArgValAlaMetGluLysIleProValSerAlaPhe 40  
DB 115 CAAGGAGGTGGGTGAGGAAATCCAGAGTGGCATGGAGAAATTCAGTGTCCAGATTTC 174  
QY 41 LeuLeuLeuValAlaLeuSerTyrThrLeuAlaArgAspThrThrValLysProGlyAla 60  
DB 175 TTGCTCTTGTGGCCCTCTCTACACTCTGGCCAGAGATACACAGTCAAACTGGAGCC 234  
QY 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGly 80  
DB 235 AAAAAGGACACAAAGACTCTCGACCCAACTGCCAGACCTCTCCAGAGGTTGGGT 294  
QY 81 AspGlnLeuIleTrpThrClnThrTyrGluGluAlaLeuTyrLysSerLysThrSerAsn 100  
DB 295 GACCAACTCATCTGACACTCAGACATATGAAGAAGCTCTATATAAATCCAAAGCAAGCAAC 354  
QY 101 LysProLeuMetIleIleHisHisLeuAspGluCysProHisSerGlnAlaLeuLysLys 120  
DB 355 AAACCTTGATGATTATTATCATCACTTGATGAGTGGCCACACAGTCAAGCTTTAAAGAAA 414  
QY 121 ValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluGlnPheValLeuLeuAsnLeu 140  
DB 415 GTGTTTGTGTAATAAAGAAATCCAGAAATGGCAGAGCACTTTGTCTCTCAATCTG 474  
QY 141 ValTyrGluThrThrAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMet 160  
DB 475 GTTATGAACAACACTGACAAACACCTTTCTCTGTGTCAGTATGTCCCGAGGATTATG 534  
QY 161 PheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyr-SerAsnArgLeu 180  
DB 535 TTTGTTGACCCATCTCTACAGTTAGAGCCGATATCACTGGAAGATATTCAATCGTCTC 594  
QY 181 TyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLysLysAlaLeuLys 200  
DB 595 TATGCTTACGAACCTGCAGATACAGCTCTGTTGCTTGACCAATCAATGAAGAAGCTCTCAAG 654  
QY 201 LeuLeuLysThrGluLeu 206  
DB 655 TTGCTGAAGACTGAATTG 672

RESULT 13

US-10-245-013-27

; Sequence 27, Application US/10245013

; Publication No. US20030186373A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Eaton, Dan

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Goddard, Audrey

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Smith, Victoria

; APPLICANT: Stephan, Jean-Phillippe

; APPLICANT: Watanabe, Colin

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; APPLICANT: Fong, Sherman

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P363081C96

; CURRENT FILING DATE: 2002-09-16

; PRIOR APPLICATION NUMBER: 10/197942

; PRIOR FILING DATE: 2002-07-18

; PRIOR APPLICATION NUMBER: 60/059114

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/063046

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/065027

; PRIOR FILING DATE: 1997-11-10

; PRIOR APPLICATION NUMBER: 60/079689

; PRIOR FILING DATE: 1998-03-27

; PRIOR APPLICATION NUMBER: 60/086478

; PRIOR FILING DATE: 1998-05-22

; PRIOR APPLICATION NUMBER: 60/087607

; PRIOR FILING DATE: 1998-06-02

; PRIOR APPLICATION NUMBER: 60/089801

; PRIOR FILING DATE: 1998-06-18

; PRIOR APPLICATION NUMBER: 60/090557

; PRIOR FILING DATE: 1998-06-24

; PRIOR APPLICATION NUMBER: 60/090689

; PRIOR FILING DATE: 1998-06-25

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 116

; SEQ ID NO 27

; LENGTH: 920

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-245-013-27

Alignment Scores:

Pred. No.: 1.33e-130 Length: 920  
Score: 1025.00 Matches: 203  
Percent Similarity: 98.54% Conservatives: 0  
Best Local Similarity: 98.54% Mismatches: 3  
Query Match: 96.43% Indels: 1  
DB: 12 Gaps: 0

US-09-674-266A-181 (1-206) x US-10-245-013-27 (1-920)

QY 1 ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgArgLeuThr 20  
DB 56 AGACTCAGCTGTGCTGGCACACTCAGAAGCTT-GGACCGCATCTAGCCGCGACTCACA 114  
QY 21 GlnGlyArgTrpValArgLysSerArgValAlaMetGluLysIleProValSerAlaPhe 40  
DB 115 CAAGGAGGTGGGTGAGGAAATCCAGAGTGGCATGGAGAAATTCAGTGTCCAGATTTC 174  
QY 41 LeuLeuLeuValAlaLeuSerTyrThrLeuAlaArgAspThrThrValLysProGlyAla 60  
DB 175 TTGCTCTTGTGGCCCTCTCTACACTCTGCCAGAGATACACAGTCAAACTGGAGCC 234  
QY 61 LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGly 80  
DB 235 AAAAAGGACACAAAGACTCTCGACCCAACTGCCAGACCTCTCCAGAGGTTGGGT 294  
QY 81 AspGlnLeuIleTrpThrClnThrTyrGluGluAlaLeuTyrLysSerLysThrSerAsn 100  
DB 295 GACCAACTCATCTGACACTCAGACATATGAAGAAGCTCTATATAAATCCAAAGCAAGCAAC 354  
QY 101 LysProLeuMetIleIleHisHisLeuAspGluCysProHisSerGlnAlaLeuLysLys 120  
DB 355 AAACCTTGATGATTATTATCATCACTTGATGAGTGGCCACACAGTCAAGCTTTAAAGAAA 414

121	ValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluGlnPheValLeuLeuAsnLeu	140
415	GTGTTTGCTGAAATAAAGAAATCCAGAAATTTGCAGAGCAGATTTGTCTCTCCCTCAATCTGT	474
141	ValTyrGluThrThrAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMet	160
475	GTTTATGAACAACACTGACANACACCTTCTCTGATGGCCAGTATGTCCCAGGANTATG	534
161	PheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnArgLeu	180
535	TTTGTTGACCCATCTCTGACAGTTAGAGCCCATATCACTGGAAGATATTCAAATCGTCTC	594
181	TyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspHisMetLysLysAlaLeuLys	200
595	TATGCTTTAGCAACCTTCGAGATACAGCTCTGTGTGTGACACATGAAAGAAAGCTCTCAAG	654
201	LeuLeuLysThrGluLeu	206
655	TTGCTGAAGACTGAATG	672

## RESULT 14

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US-10-245-103-27
; Sequence 27, Application US/10245103
; Publication No. US20030068778A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Matanbe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630RIC112
; CURRENT APPLICATION NUMBER: US/10/245,103
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 27
; LENGTH: 920
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-245-103-27

```

Alignment Scores:	
Pred. No.:	1.33e-130
Score:	1025.00
Length:	920
Matches:	203

Percent Similarity:	98.54%	Conservative:	0
Best Local Similarity:	98.54%	Mismatches:	3
Query Match:	96.43%	Indels:	1
DB:	14	Gaps:	0
US-09-674-266A-181 (1-206) x US-10-245-103-27 (1-920)			
Qy	1	ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgArgLeuThr	20
Db	56	AGACTCAGCTGTGTGGCACACTCAGAAAGCTT-GGACCGCATCTCTAGCGCGGACTCACA	114
Qy	21	GlnGlyArgTrpValArgLysSerArgValAlaMetGluLysValIleProValSerAlaPhe	40
Db	115	CAAGCGAGGTGGGTGGAGAAATCCAGAGTTCCTATGGAGAAATTCCTAGTGTCCAGATTC	174
Qy	41	LeuLeuLeuValAlaLeuSerTyrThrLeuAlaArgAspThrThrValLysProGlyAla	60
Db	175	TTGCTCTTGTGGCCCTCTCTCACACTCTGGCCAGAGATACCACAGTCAAACTCGAGCC	234
Qy	61	LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTrpGly	80
Db	235	AAAAGAGACAAAGGACTCTCGACCCAAATGCCCCAGACCCCTCTCCAGAGGTTGGGGT	294
Qy	81	AspGlnLeuIleTprThrGlnThrTyrGluGluAlaLeuTyrLysSerLysThrSerAsn	100
Db	295	GACCACTCATCTGGACTCAGACATATGAAAGAGCTCTATATAATCCNAGACNAGCAAC	354
Qy	101	LysProLeuMetIleIleHisLeuAspGluCysProHisSerGlnAlaLeuLysLys	120
Db	355	AAACCTTGATGATTATTTCATCACTTGGATGAGTGCCACACAGTCAAGCTTTAAAGAA	414
Qy	121	ValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluInPheValLeuLeuAsnLeu	140
Db	415	GTGPTTCTGAAAAATAAGAAATCCAGAAATGGCAGACAGCTTTGTCTCTCTCAATCTG	474
Qy	141	ValTyrGluThrThrAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMet	160
Db	475	GTTTATGAACAACCTGACAAACACCTTTCTCTGATGCCAGTATGTCCCCAGGATTATG	534
Qy	161	PheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnArgLeu	180
Db	535	TTTGTTCACCCATCTCTGACAGTTAGAGCCGATATCATCTGGAAGATATTTCAAATCGTCTC	594
Qy	181	TyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLysLysAlaLeuLys	200
Db	595	TATGCTTACGNACCTGGAGATACAGCTCTGTGTGCTTGACAACTGACNAGAAAGCTCTCAAG	654
Qy	201	LeuLeuLysThrGluLeu	206
Db	655	TTGCTGAAGACTGAATTG	672

## RESULT 15

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RES001 13
US/10-245-107-27
: Publication 27, Application US/10245107
: Publication No. US20030068779A1
:
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
: APPLICANT: Eaton, Dan
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Goddard, Audrey
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin
: APPLICANT: Smith, Victoria
: APPLICANT: Stephan, Jean-Phillippe
: APPLICANT: Watanbe, Colin
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: APPLICANT: Fong, Sherman
: TITLE OF INVENTION: SECURED AND TR
: ACIDS ENCODING
: FILE OF INVENTION: P3630R1C71
: FILE REFERENCE: P3630R1C71
: CURRENT APPLICATION NUMBER: US/10/2
: CURRENT FILING DATE: 2002-09-16

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;; PRIOR APPLICATION NUMBER: 10/197942  
;; PRIOR FILING DATE: 2002-07-18  
;; PRIOR APPLICATION NUMBER: 60/059114  
;; PRIOR FILING DATE: 1997-09-17  
;; PRIOR APPLICATION NUMBER: 60/063046  
;; PRIOR FILING DATE: 1997-10-24  
;; PRIOR APPLICATION NUMBER: 60/065027  
;; PRIOR FILING DATE: 1997-11-10  
;; PRIOR APPLICATION NUMBER: 60/079689  
;; PRIOR FILING DATE: 1998-03-27  
;; PRIOR APPLICATION NUMBER: 60/086478  
;; PRIOR FILING DATE: 1998-05-22  
;; PRIOR APPLICATION NUMBER: 60/087607  
;; PRIOR FILING DATE: 1998-06-02  
;; PRIOR APPLICATION NUMBER: 60/089801  
;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: 60/090557  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090689  
;; PRIOR FILING DATE: 1998-06-25  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 116  
;; SEQ ID NO 27  
;; LENGTH: 920  
;; TYPE: DNA  
;; ORGANISM: Homo Sapien  
US-10-245-107-27

Alignment Scores:  
Pred. No.: 1.33e-130 Length: 920  
Score: 1025.00 Matches: 203  
Percent Similarity: 98.54% Conservative: 0  
Best Local Similarity: 98.54% Mismatches: 3  
Query Match: 96.43% Indels: 1  
DB: 14 Gaps: 0

US-09-674-266a-181 (1-206) x US-10-245-107-27 (1-920)

```
QY      1  ArgLeuSerCysAlaGlyThrLeuSerGlySerGlyProHisProSerArgArgLeuThr 20
DB      56  AGACTCAGCTGTGCTGGACACTCAGAACGTT-GGACCCGATCCTAGCCGCGACTCACA 114

QY      21  GlnGlyArgTyrValArgLysSerArgValAlaMetGluLysIleProValSerAlaPhe 40
DB      115  CAAGCAGCTGGGTGAGGAATCCAGAGTTGCCATGGAGAAATTCACGTGTCAGCAATC 174

QY      41  LeuLeuLeuValAlaLeuSerTyrThrLeuAlaArgAspThrThrValLysProGlyAla 60
DB      175  TTGCTCCTTGTGGCCCTCTCTACACTCTGGCCAGAGATACCACAGTCAAACCTGGAGCC 234

QY      61  LysLysAspThrLysAspSerArgProLysLeuProGlnThrLeuSerArgGlyTyrGly 80
DB      235  AAAAAGGACAAAGAGACTCTCGACCAAACTGCCCCAGACCCCTCTCCAGAGGTGGGGT 294

QY      81  AspGlnLeuIleTyrThrGlnThrTyrGluGluAlaLeuTyrLysSerLysThrSerAsn 100
DB      295  GACCAACTCATCTGGACTCAGACATATGAAGAGCTCTATATAATCCAGACAGCAAC 354

QY      101  LysProLeuMetIleIleHisLysLeuAspGluCysProHisSerGlnAlaLeuLysLys 120
DB      355  AAACCCCTTGATGATTATTCATCATTGGATGAGTGCCACACAGTCAAGCTTTAAAGAA 414

QY      121  ValPheAlaGluAsnLysGluIleGlnLysLeuAlaGluGlnPheValLeuLeuAsnLeu 140
DB      415  GTGTTTGCTGAAAATAAAGAAATCCAGAAATGGCAGAGCAGTTGTCTCTCTCAATCTG 474

QY      141  ValTyrGluThrThrAspLysHisLeuSerProAspGlyGlnTyrValProArgIleMet 160
DB      475  GTTTATGAACAACACTGACAAACACCTTTCTCTGATGGCCAGTATGTCCCCAGGATTATG 534

QY      161  PheValAspProSerLeuThrValArgAlaAspIleThrGlyArgTyrSerAsnArgLeu 180
DB      535  TTTGTTGACCCATCTCTGACAGTTAGAGCCGATATCCTCTGGAAGATATTCAAAATCGTCTC 594
```

```
QY      181  TyrAlaTyrGluProAlaAspThrAlaLeuLeuLeuAspAsnMetLysLysAlaLeuLys 200
DB      595  TATGCTTACGAACCTGCAGATACAGCTCTGTGCTTGACACATGAGAAAGCTCTCAAG 654

QY      201  LeuLeuLysThrGluLeu 206
DB      655  TTGCTGAAGACTGAATTG 672
```

Search completed: November 30, 2003, 05:00:53  
Job time : 311 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2003, 15:52:53 ; Search time 21 Seconds  
(without alignments)  
943.369 Million cell updates/sec

Title: US-09-674-266A-181  
Perfect score: 1063  
Sequence: 1 RLSCAGTSLSGSPHSRLT.....DTALLDNMKALKLKTTEL 206

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues  
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	899	84.6	175	JE0350	Anterior gradient-
2	199	18.7	186	T31643	hypothetical prote
3	119	11.2	150	D63100	probable protein d
4	87.5	8.2	458	S50919	hypothetical prote
5	87	8.2	348	G72016	probable disulfide
6	87	8.2	348	C86607	disulfide bond iso
7	85.5	8.0	1830	S19188	myosin-V - chicken
8	84.5	7.9	1151	AG1717	probable peptidogl
9	84	7.9	771	S51421	hypothetical prote
10	83.5	7.9	217	T37859	probable transcrip
11	83.5	7.9	918	C96829	unknown protein F1
12	83	7.8	479	T40683	cell cycle protein
13	83	7.8	507	S56143	cell cycle protein
14	82.5	7.8	788	C70441	lipote-protein li
15	81.5	7.7	893	GS9431	phosphatidylinosit
16	81.5	7.7	970	S29069	inositol polyphosp
17	81.5	7.7	1158	T50454	probable rho1 Gdp-
18	81.5	7.7	1397	T10466	DNA topoisomerase
19	81	7.6	610	T22909	hypothetical prote
20	81	7.6	635	T23874	hypothetical prote
21	80	7.5	154	F82633	probable protein d
22	80	7.5	259	A67640	F14023.14 [impor
23	80	7.5	847	S53947	hypothetical prote
24	79.5	7.5	277	T37629	hypothetical prote
25	79.5	7.5	301	G71929	GTP-binding protei
26	79.5	7.5	642	F83718	ABC transporter (A
27	79.5	7.5	921	F84593	hypothetical prote
28	79	7.4	477	T37791	probable rna polym
29	79	7.4	510	S43516	carboxypeptidase C

30	78.5	7.4	280	2	AG9590	shikimate 5-dehydr
31	78.5	7.4	917	2	T05430	hypothetical prote
32	78.5	7.4	1033	2	A96714	hypothetical prote
33	78.5	7.4	1262	2	I48855	tripeptidyl-peptid
34	78.5	7.4	1570	2	AC2012	hypothetical prote
35	78	7.3	337	2	S06956	segmentation prote
36	78	7.3	1828	2	B59254	myosin heavy chain
37	78	7.3	1853	1	A46761	myosin heavy chain
38	78	7.3	1855	2	A59254	myosin heavy chain
39	76.5	7.2	985	2	E59850	formate dehydrogen
40	76.5	7.2	1025	2	T10259	RNA-directed DNA p
41	76	7.1	166	2	E2018	thioredoxin disulf
42	76	7.1	166	2	D86606	thioredoxin disulf
43	76	7.1	367	2	T39574	oligopeptide-bindi
44	76	7.1	543	1	F64871	probable peptide A
45	76	7.1	583	2	E75529	

ALIGNMENTS

RESULT 1

JE0350  
Anterior gradient-2 - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 21-Jul-2000  
C:Accession: JE0350  
R:Thompson, D.A.; Weigel, R.J.  
Biochem. Biophys. Res. Commun. 251, 111-116, 1998  
A:Title: hAG-2, the human homologue of the Xenopus laevis cement gland gene XAG-2, is co-expressed with estrogen receptor (ER) in breast cancer cell.  
A:Reference number: JE0350; MUID:99009231; PMID:9790916  
A:Accession: JE0350  
A:Molecule type: mRNA  
A:Residues: 1-175 <THO>  
A:Cross-references: GB:AF007791; NID:g3779196; PIDN:AAC77358.1; PID:g3779197  
C:Comment: This protein is coexpressed with estrogen receptor (ER) in breast cancer cell.  
C:Genetics:  
A:Gene: hAG-2  
C:Superfamily: human anterior gradient-2

Query Match	84.6%	Score	899	DB	2	Length	175
Best Local Similarity	100.0%	Pred. No.	3.1e-74				
Matches	175	Conservative	0	Mismatches	0	Indels	0
Qy	32	MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQYEE	91				
Db	1	MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQYEE	60				
Qy	92	ALYKSKTSNKPLMIHHLDECPHSQALKKVFPAENKEIQKLAEQFVLLNLVYETTDKHLSP	151				
Db	61	ALYKSKTSNKPLMIHHLDECPHSQALKKVFPAENKEIQKLAEQFVLLNLVYETTDKHLSP	120				
Qy	152	DGQVPRIMFVDPSTVVRADITGRYSNRLYAYEPADTALLDNMKALKLKTTEL	206				
Db	121	DGQVPRIMFVDPSTVVRADITGRYSNRLYAYEPADTALLDNMKALKLKTTEL	175				

RESULT 2

T31643  
hypothetical protein Y57A10A.u - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 20-Jun-2000  
C:Accession: T31643  
R:Smyle, R.  
submitted to the EMBL Data Library, September 1999  
A:Reference number: Z21048  
A:Accession: T31643  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-186 <WIL>  
A:Cross-references: EMBL:AL117195; PIDN:CAB55026.1; CESP:Y57A10A.u  
A:Experimental source: clone Y57A10A  
C:Genetics:

A;Gene: CESP:Y57A10A.u  
A;Introns: 70/1  
C;Superfamily: human anterior gradient-2

Query Match 18.7%; Score 199; DB 2; Length 186;  
Best Local Similarity 30.0%; Pred. No. 1.1e-10;  
Matches 51; Conservative 38; Mismatches 57; Indels 24; Gaps 6;

QY 41 LLLVALSYTLARDTTVPKAGKDTKDSRPKLPQTLSRGWGDOLIWTQTYEALYKSKTSN 100

DB 4 LLLAL-----VSASAYASPDKTKIQNPLARGFGDDIAWVK-WEDATETALDITD 53

QY 101 KPLMIHHLDECPSQALKVFAEN---KEIQKLAQFVLLNLV--YETTDKHLSPDGOY 155

DB 54 KPFLHLHKSCHACKALKTKTFQSNNAKFAKFLSEHFVWVNTEDDDPEPEEYRPDCKY 113

QY 156 VPRIMFVDPSTVRADITGRYSNRL-----YAYEPADTALLLNNMKALK 200

DB 114 IPRLLFLDKN---GDLLEQFKNKAEYKKNYAYVYSSPADILNSMKDVLK 159

RESULT 3  
D69100  
probable protein disulfide-isomerase (EC 5.3.4.1) MTH1745 [similarity] - Methanobacterium  
C;Species: Methanobacterium thermoautotrophicum  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 15-Sep-2000  
C;Accession: D69100

R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;  
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.  
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
J. Bacteriol. 179, 7135-7155, 1997

A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funch

A;Reference number: A69000; MUID:98037514; PMID:9371463

A;Accession: D69100

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-150 <MTH>

A;Cross-references: GB:AE000930; GB:AE000666; NID:g2622872; PIDN:AAB86215.1; PID:g262287

A;Experimental source: strain Delta H

C;Genetics:

A;Gene: MTH1745

C;Keywords: intramolecular oxidoreductase; isomerase

Query Match 11.28; Score 119; DB 2; Length 150;

Best Local Similarity 27.18; Pred. No. 0.0015;

Matches 35; Conservative 28; Mismatches 46; Indels 20; Gaps 4;

QY 39 AFLLLVALSYTLARDTTVPKAGKDTKDSRPKLPQTLSRGWGDOLIWTQTYEALYKSKT 98

DB 19 AGLSLVLIITV-----QPRVPSLTDEKD-LKWYTEHDEAIKEASR 60

QY 99 SNKPLMIHHLDECPSQALKVFAENKEIQ-KLAQFVLLNLVYETTDKHLSPDGOY-V 156

DB 61 TGNVNFVFSASWCPACQKLESETLQNTVEQRLAEDFIAVKIDVDTSPALSSRYRIYGV 120

QY 157 PRIMFVDPSS 165

DB 121 PTVIIDPS 129

RESULT 4  
S50919  
hypothetical protein YMR191w - yeast (Saccharomyces cerevisiae)  
N;Alternate names: hypothetical protein YW9646.03  
C;Species: Saccharomyces cerevisiae  
C;Date: 10-Feb-1995 #sequence\_revision 12-May-1995 #text\_change 19-Apr-2002  
C;Accession: S50919; S55721

R;Pearson, D.; Bowman, S.

submitted to the EMBL Data Library, January 1995

A;Reference number: S50919

A;Accession: S50919

A;Molecule type: DNA

A;Residues: 1-458 <PEA>

A;Cross-references: EMBL:Z47815; NID:g642280; PIDN:CAA87812.1; PID:g642283; MIPS:YMR191w  
R;Gangloff, S.; McDonald, J.P.; Bendixen, C.; Arthur, L.; Rothstein, R.  
Mol. Cell. Biol. 14, 8391-8398, 1994

A;Title: The yeast type I topoisomerase Top3 interacts with Sgs1, a DNA helicase homolog

A;Reference number: A56359; MUID:95059068; PMID:7969174

A;Accession: S55721

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-127, 'Y', 129-131, 'LALG', 136-249 <CAN>

A;Cross-references: EMBL:U22341; NID:g726277; PIDN:AAB60288.1; PID:g726278

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1995

C;Genetics:

A;Map position: 13R

A;Cross-references: SGD:S0004803

C;Superfamily: Saccharomyces cerevisiae hypothetical protein YMR191w

Query Match 8.2%; Score 87.5; DB 2; Length 458;

Best Local Similarity 20.1%; Pred. No. 4.5;

Matches 55; Conservative 35; Mismatches 74; Indels 109; Gaps 13;

QY 15 PSRLTQGG-----RWYKSRVAMEKIPVSAFLLLVALS----- 47

DB 82 PTERNAVGGNNMSWLMRGRVHLRQITKSLDRTLISLHGNSFHSQYNNRNFTVWTKSLFE 141

QY 48 -----YTLARDTTVPKAGKDTK-----DSRPKLPQTLSRG---W---GD 81

DB 142 ASTAFRRASGLTVSPLTRGCIARPDHFRPVPNVSKFASPRVPKGPAGRLFTWNNMTTSK 201

QY 82 QLIWTQTYEALYK---SKTSNKPLMI-----IHLDECPSHQ--- 116

DB 202 RLLGQRAYSTSSIKFTQEAANNMTISLRGFFNSLGLGNCSSNSKAYQNASNVTSKQD 261

QY 117 -----ALKKV-----FAENKEIQKLAQFVLLNLVYETTDKHLSPDGOYV----- 156

DB 262 HVQPVALKKQKQDINFIRNLEFKMK--TQNEVVDTSAYIWEKPGSYIEFTISEFNV 319

QY 157 -----PRIMFVDPSTVRADITGRYSNRLYAYE 184

DB 320 NGTFSAPLFLDPSLL--ADLDEMIRN--YKYE 348

RESULT 5

G72016

probable disulfide bond isomerase - Chlamydomophila pneumoniae (strains CWL029 and AR39)

C;Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae

C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 11-May-2000

C;Accession: G72016; B81523

R;Kelman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;

Nature Genet. 21, 385-389, 1999

A;Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

A;Reference number: A72000; MUID:99206606; PMID:10192388

A;Accession: G72016

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-348 <ARN>

A;Cross-references: GB:AE001673; GB:AE001363; NID:g4377252; PIDN:AAD19071.1; PID:g437725

A;Experimental source: strain CWL029

R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, I.;

C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,

Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A;Reference number: A81500; MUID:20150255; PMID:10684935

A;Accession: B81523

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-348 <REA>

A;Cross-references: GB:AE002251; GB:AE002161; NID:g7189833; PIDN:AAF38711.1; PID:g7189840

A;Experimental source: strain AR39, HL cells

C;Genetics:

A;Gene: CPN0933; CP0928

Query Match 8.2%; Score 87; DB 2; Length 348;

Best Local Similarity 25.0%; Pred. No. 3.5;

A;Title: cDNA encoding the chicken ortholog of the mouse dilute gene product. Sequence  
A;Reference number: S29249; MUID:93012002; PMID:1383040  
A;Accession: S29249  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-1142,1144-1830 <S>  
A;Cross-references: EMBL:X67251; NID:G63364; PIDN:CAA47673.1; PID:G63365  
C;Comment: The neck domain comprises six approximately 23-residue tandem repeats; this  
C;Superfamily: myosin MYO2; myosin motor domain homology  
C;Keywords: actin binding; ATP; brain; coiled coil; nucleotide binding; P-loop; phospho;  
F;72-752/Domain: myosin motor domain homology <MMOT>  
F;163-170/Region: nucleotide-binding motif A (P-loop)  
F;645-666/Region: actin binding #status predicted  
F;765-909/Domain: neck #status predicted <NEC>  
F;912-1420/Domain: coiled coil #status predicted <COR>  
F;1421-1830/Domain: carboxyl-terminal domain #status predicted <CTD>  
F;169/Binding site: ATP (lvs) #status predicted  
F;1735/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 8.0%; Score 85.5; DB 1; Length 1830;  
Best Local Similarity 28.1%; Pred. No.38;  
Matches 27; Conservative 21; Mismatches 41; Indels 7; Gaps 3;

Qy 63 DTKDSRPKLPTQLSRGSGDGLIWTQTYEALY-KKSTSNKPLMIITHLDECH--SQALK 119  
Db 507 DLLDECKMPKGSDDTWAQKLNYNTHLNCALFEKPLSNKFAIIKHFDKVEYQCSEGLE 566  
Qy 120 K----VFAENKEIQKLAEQFVLLNLVYETTDKHLSP 151

567 KNDQIVIEQIKVLKSSKRAKFLPDLFQDEERNAISP 602

RESULT 8  
AG1717  
probable peptidoglycan bound protein (LPXTG motif) lin283 [imported] - *Listeria innocua*  
C;Species: *Listeria innocua*  
C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001  
C;Accession: AG1717  
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.

```

A;Authors: Kreif, J.; Kuhn, M.; Kunat, F.; Kurapkat, G.; Maqueno, E.; Maitournam, A.; M.
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A; Cite: Comparative genomics of Listeria species.
A;Title: Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1717
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1151 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC97511.1; PID:g16144795; GSPDB:GN00178
A;Experimental source: strain Clp11262
C;Genetics:
A;Gene: lin2283

Query Match 7.9%; Score 84.5; DB 2; Length 1151;
Best Local Similarity 22.6%; Pred. No.25;
Matches 44; Conservative 31; Mismatches 51; Indels 67; Gaps 10;

QY 50 LARDTTVKEGAKK--DTKDSRKLPTQLSRGWDQLITWQ-----TYE 90
Db 961 VALDDSVAPVTVOYVDONHOKTASPETLTGAGYGEKFTAKOKKITNTVTLVKTPANVSGETN 1020

```

[illegible]

Db 1112 ADNVEKSAKLPT 1124

RESULT 9  
S51421  
hypothetical protein YLR176c - yeast (Saccharomyces cerevisiae)  
N:Alternate names: hypothetical protein L9470.18  
C:Species: Saccharomyces cerevisiae  
C>Date: 23-Feb-1995 #sequence\_revision 12-May-1995 #text\_change 06-Feb-1998  
C:Accession: S51421  
R:Wohldmann, P.  
submitted to the EMBL Data Library, November 1994  
A:Description: The sequence of *S. cerevisiae* cosmid 9470.  
A:Reference number: S51414  
A:Accession: S51421  
A:Molecule type: DNA  
A:Residues: 1-771 <WOH>  
A:Cross-references: EMBL:U17246; NID:9577192; PID:9577210; MIPS:YLR176C  
C:Genetics:  
A:Gene: SGD:RFX1  
A:Cross-references: SGD:S0004166; MIPS:YLR176C  
A:Map position: 12R

Query Match 7.9%; Score 84; DB 2; Length 771;  
Best Local Similarity 25.7%; Pred. No. 18;  
Matches 47; Conservative 29; Mismatches 67; Indels 40; Gaps 8;

Qy 8 LSGSGP-----HPSRLTQGR-----WVRKSRVAMEKIPVSFLLLVALSITLAR 52  
Db 89 LIGSGSGHKPSPTPTQPPAQATQRPATYSVPASISLNRSSAYPLSFKEETLNN 148  
Qy 53 D--TTVK-----PGAKKTKDSRPKLPQTLSPRGWDQLIWTQTYEALYKSKTSNKP 102  
Db 149 NPPTAARTNTPSPISPTKQKTSQSKRISISIRNTQETIIAKQIAEN--NKSRTIEY 206  
Qy 103 LMIITH-----LDECPHSQALKVFAENKEIQKLAEQFVLLNLVYETTDKHLSPDGQY 155  
Db 207 AQIVKHAIEKVLNSDQNTSKAALQAEQNERER--QVALLWLMKNCKSQHDS----Y 260  
Qy 156 VPR 158  
Db 261 VPR 263

RESULT 10  
T37859  
probable transcription factor - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
C:Accession: T37859  
R:Daylin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.  
submitted to the EMBL Data Library, February 1996  
A:Reference number: 221750  
A:Accession: T37859  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-217 <DEV>  
A:Cross-references: EMBL:Z69795; PIDN:CAA93690.1; GSPDB:GN00066; SPDB:SPAC1768.07  
A:Experimental source: strain 972h-; cosmid c1768  
C:Genetics:  
A:Gene: SPDB:SPAC1768.07  
A:Map position: 1

Query Match 7.9%; Score 83.5; DB 2; Length 217;  
Best Local Similarity 20.6%; Pred. No. 4.1;  
Matches 42; Conservative 33; Mismatches 80; Indels 49; Gaps 8;

Qy 14 HPSRLTQG-----BWVRKSRVAMEKIPVSFLLLVALSITLARDTTVKPGAKKTKD 66  
Db 39 HTRIFVEGVGDGDISKWVRK-----VVPKL-----HDTYNNP---TKTIE 76  
Qy 67 SRPKLPQTLSPRGWDQLIWTQTYEALYKSKTSNKPMLIIHLDCEPHSQALKVFAENK 126

Db 1112 ADNVEKSAKLPT 1124

RESULT 9  
S51421  
hypothetical protein YLR176c - yeast (Saccharomyces cerevisiae)  
N:Alternate names: hypothetical protein L9470.18  
C:Species: Saccharomyces cerevisiae  
C>Date: 23-Feb-1995 #sequence\_revision 12-May-1995 #text\_change 06-Feb-1998  
C:Accession: S51421  
R:Wohldmann, P.  
submitted to the EMBL Data Library, November 1994  
A:Description: The sequence of *S. cerevisiae* cosmid 9470.  
A:Reference number: S51414  
A:Accession: S51421  
A:Molecule type: DNA  
A:Residues: 1-771 <WOH>  
A:Cross-references: EMBL:U17246; NID:9577192; PID:9577210; MIPS:YLR176C  
C:Genetics:  
A:Gene: SGD:RFX1  
A:Cross-references: SGD:S0004166; MIPS:YLR176C  
A:Map position: 12R

Query Match 7.9%; Score 84; DB 2; Length 771;  
Best Local Similarity 25.7%; Pred. No. 18;  
Matches 47; Conservative 29; Mismatches 67; Indels 40; Gaps 8;

Qy 8 LSGSGP-----HPSRLTQGR-----WVRKSRVAMEKIPVSFLLLVALSITLAR 52  
Db 89 LIGSGSGHKPSPTPTQPPAQATQRPATYSVPASISLNRSSAYPLSFKEETLNN 148  
Qy 53 D--TTVK-----PGAKKTKDSRPKLPQTLSPRGWDQLIWTQTYEALYKSKTSNKP 102  
Db 149 NPPTAARTNTPSPISPTKQKTSQSKRISISIRNTQETIIAKQIAEN--NKSRTIEY 206  
Qy 103 LMIITH-----LDECPHSQALKVFAENKEIQKLAEQFVLLNLVYETTDKHLSPDGQY 155  
Db 207 AQIVKHAIEKVLNSDQNTSKAALQAEQNERER--QVALLWLMKNCKSQHDS----Y 260  
Qy 156 VPR 158  
Db 261 VPR 263

RESULT 10  
T37859  
probable transcription factor - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
C:Accession: T37859  
R:Daylin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.  
submitted to the EMBL Data Library, February 1996  
A:Reference number: 221750  
A:Accession: T37859  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-217 <DEV>  
A:Cross-references: EMBL:Z69795; PIDN:CAA93690.1; GSPDB:GN00066; SPDB:SPAC1768.07  
A:Experimental source: strain 972h-; cosmid c1768  
C:Genetics:  
A:Gene: SPDB:SPAC1768.07  
A:Map position: 1

Query Match 7.9%; Score 83.5; DB 2; Length 217;  
Best Local Similarity 20.6%; Pred. No. 4.1;  
Matches 42; Conservative 33; Mismatches 80; Indels 49; Gaps 8;

Qy 14 HPSRLTQG-----BWVRKSRVAMEKIPVSFLLLVALSITLARDTTVKPGAKKTKD 66  
Db 39 HTRIFVEGVGDGDISKWVRK-----VVPKL-----HDTYNNP---TKTIE 76  
Qy 67 SRPKLPQTLSPRGWDQLIWTQTYEALYKSKTSNKPMLIIHLDCEPHSQALKVFAENK 126

Db 77 SPPF--EVIETGWGEFDIMVRIF-----FAPEAHEKALTYHHLKHPYGPMBEMKASGG 130

Qy 127 EIQLAEQFVLLNLVYETTDKHLSP-----DGOVPRIMFVDPSTLRADITGRYSNRLYA 182

Db 131 LVESVQVEIEVFNEPEFTYTKLSQNPIDGHD-----GLAVESEDPHPFQOQLEQ 180

Qy 183 YEPADTALLDNNMKKALKLKTTEL 206

Db 181 DEADKLDFAIQEVKVTIEMVYKQV 204

RESULT 11  
C96829  
unknown protein F19K16.21 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C:Accession: C96829  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.;  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: C96829  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-918 <STO>  
A:Cross-references: GB:AE005173; NID:96453864; PIDN:AAF09048.1; GSPDB:GN00141  
C:Genetics:  
A:Gene: F19K16.21  
A:Map position: 1

Query Match 7.9%; Score 83.5; DB 2; Length 918;  
Best Local Similarity 21.3%; Pred. No. 24;  
Matches 46; Conservative 41; Mismatches 76; Indels 53; Gaps 9;

Qy 36 PVSFALLVALSYTL-----ARDTTVKPGAKKD---TKDSRPKLPQTLSPRGWDQLIWT 86

Db 149 PQSQILLESSEYSLOTPESSGYKTSLOPNEKLEMTASQDSQPEQPK--SEASESQPEDS 206

Qy 87 QTYEALYKSKTSNKPML-----IIHLDCEPHSQALKVFAENKEIQKLAEQFVLL--- 138

Db 207 EAKEVTVENKDTVHSPVLDQCHKITTYMDETTNQ---EILGENLEGRSTSKNFEVSPDIN 263

Qy 139 -----NLVYETTDKHLSPDGQYVPR-----IMFVDPSTLRADI--- 172

Db 264 HVNRIEVPVHPSLIFESDG---SPYESIPFKSSSEISERIVDFVSRIDSLRLOTSEL 320

Qy 173 --TGRYSNRLYAYEPADTALLDNNMKKALKLKTTEL 206

Db 321 NESQSSSATNVSDSADVILELEKTKKEIKLENAL 356

RESULT 12  
T40683  
cell cycle protein kinase hsk1 - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Jan-2000  
C:Accession: T40683  
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Wedler, H.; Kutzner, M.; Wambutt, R.  
submitted to the EMBL Data Library, January 1999  
A:Reference number: 221944  
A:Accession: T40683  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-479 <LYN>  
A:Cross-references: EMBL:AL035263; PIDN:CAB38417.1; GSPDB:GN00067; SPDB:SPBC776.12c  
A:Experimental source: strain 972h-; cosmid c776

C:Genetics:  
A:Gene: SPDB:SPBC776.12c  
A:Map position: 2  
A:Introns: 77/1, 92/2, 331/1  
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

Query Match 7.8%; Score 83; DB 2; Length 479;  
Best Local Similarity 22.4%; Pred. No. 12;  
Matches 28; Conservative 24; Mismatches 55; Indels 18; Gaps 5;

QY 83 LIWTQTYEALYKSTNKP-----LMIHHLDECPHSQALKKVFPAENKEIQKLAQFVLL 138  
DB 352 ILWAGSGASIVKEKLRHKPSQERLCLDFLEKCLDNCNKRISAE-----EALDHDHFLYL 407

QY 139 -NLVYETTDKHLSPDQGVPRIMFVDPSTVTRADITGRYSNRLYAY---EPADTALLLDN 194  
DB 408 DNLAYEKDDDTAFDNS-----FGTSPKEDDLTAKHLSHLDLFKQSEETDEPTSLSK 461

QY 195 MKKAL 199  
DB 462 RKRSI 466

RESULT 13  
S56143  
C:Species: Schizosaccharomyces pombe  
C:Date: 28-Oct-1995 #sequence\_revision 10-Nov-1995 #text\_change 10-Dec-1999  
C:Accession: S56143; T40682  
R:Maadai, H.; Miyake, T.; Arai, K.  
EMBO J. 14, 3094-3104, 1995  
A:Title: hsk1(+), a Schizosaccharomyces pombe gene related to Saccharomyces cerevisiae C  
A:Reference number: S56143; MUID:95347336; PMID:7621824  
A:Accession: S56143  
A:Molecule type: DNA  
A:Residues: 1-507 <NAS>  
A:Cross-references: GB:D50493; NID:9807845; PIDN:BAA09087.1; PID:d1009722; PID:g807846  
A:Experimental source: strain JY2  
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Wedler, H.; Kutzner, M.; Wambutt, R.  
submitted to the EMBL Data Library, January 1999  
A:Reference number: Z1944  
A:Accession: T40682  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-507 <LYN>  
A:Cross-references: EMBL:AL035263; PIDN:CAA22885.1; GSPDB:GN00067; SPDB:SPBC776.12c  
A:Experimental source: strain 972h-; cosmid c776  
C:Genetics:  
A:Gene: hsk1; SPBC776.12c  
A:Map position: 2  
A:Introns: 77/1, 359/1  
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog  
C:Keywords: phosphotransferase; protein kinase  
F:66-404/Domain: protein kinase homology <KIN>

Query Match 7.8%; Score 83; DB 2; Length 507;  
Best Local Similarity 22.4%; Pred. No. 13;  
Matches 28; Conservative 24; Mismatches 55; Indels 18; Gaps 5;

QY 83 LIWTQTYEALYKSTNKP-----LMIHHLDECPHSQALKKVFPAENKEIQKLAQFVLL 138  
DB 380 ILWAGSGASIVKEKLRHKPSQERLCLDFLEKCLDNCNKRISAE-----EALDHDHFLYL 435

QY 139 -NLVYETTDKHLSPDQGVPRIMFVDPSTVTRADITGRYSNRLYAY---EPADTALLLDN 194  
DB 436 DNLAYEKDDDTAFDNS-----FGTSPKEDDLTAKHLSHLDLFKQSEETDEPTSLSK 489

QY 195 MKKAL 199  
DB 490 RKRSI 494

RESULT 14

C70441

lipote-protein ligase A - Aquifex aeolicus

C:Species: Aquifex aeolicus

C:Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 05-Nov-1999

C:Accession: C70441

R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.

Nature 392, 353-358, 1998

A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A:Reference number: A70300; MUID:98196666; PMID:9537320

A:Accession: C70441

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-788 &lt;AQF&gt;

A:Cross-references: GB:A5000748; NID:92983960; PIDN:AAC07512.1; PID:g2983965; GB:A500065

A:Experimental source: strain VF5

C:Genetics:

A:Gene: lplA





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 26, 2003, 15:49:13 ; Search time 18 Seconds  
(without alignments)  
538.195 Million cell updates/sec

Title: US-09-674-266A-181

Perfect score: 1063

Sequence: 1 RLSCAGTLGSGPHPSRLT.....DTALLDNMKKALKLKTTEL 206

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	448	42.1	183	XAG_XENLA	P55868 xenopus lae
2	437.5	41.2	185	NP77_XENLA	P55869 xenopus lae
3	224.5	21.1	170	TL19_MOUSE	Q9cqu0 mus musculus
4	222	20.9	172	TL19_HUMAN	O95881 homo sapien
5	87.5	8.2	458	YMS1_YEAST	P42933 saccharomyc
6	85.5	8.0	1829	MYSA_CHICK	Q02440 gallus gall
7	84	7.9	811	RFK1_YEAST	P48743 saccharomyc
8	83.5	7.9	217	YD67_SCHPO	Q10319 schizosacch
9	83	7.8	507	HSK1_SCHPO	P50582 schizosacch
10	81.5	7.7	901	OCRL_HUMAN	Q01968 homo sapien
11	81.5	7.7	1398	TOP2_PLAPK	P41001 plasmodium
12	80	7.5	339	YTH6_RHOER	P43484 rhodococcus
13	80	7.5	843	YMS1_YEAST	Q05050 saccharomyc
14	79.5	7.5	301	ERA_HELPJ	Q921w0 helicobacte
15	79	7.4	477	TFB1_SCHPO	O13745 schizosacch
16	79	7.4	510	CBP1_ORYSA	P37890 oryza sativ
17	78.5	7.4	280	AROE_BACSU	P54374 bacillus su
18	78.5	7.4	917	DMJ3_ARATH	Q04998 arabidopsis
19	78.5	7.4	1262	TPR2_MOUSE	Q64514 mus musculus
20	78.5	7.4	1828	MYSA_RAT	Q9qvf3 rattus norv
21	78	7.3	337	HAIR_DROME	P14003 drosophila
22	78	7.3	887	ITH3_RAT	Q63416 rattus norv
23	78	7.3	1853	MYSA_MOUSE	Q99104 mus musculus
24	78	7.3	1855	MYSA_HUMAN	Q99411 homo sapien
25	77	7.2	729	YP65_CAEEL	Q09214 caenorhabdi
26	76.5	7.2	524	HY11_BRAJA	P59385 bradyrhizob
27	76.5	7.2	1025	PO31_NASVI	Q03278 nasonia vit
28	76	7.1	543	OPPA_ECOLI	P23843 escherichia
29	76	7.1	1650	VIT6_CAEEL	P18948 caenorhabdi
30	76	7.1	2145	US20_CAEEL	Q9uz90 caenorhabdi
31	75.5	7.1	580	TRE2_MYCTU	Q10769 mycobacteri
32	75.5	7.1	2318	NTC3_MOUSE	Q61982 mus musculus
33	75	7.1	1694	SN_MOUSE	Q62230 mus musculus

## RESULT 1

XAG\_XENLA  
ID XAG\_XENLA STANDARD; PRT; 183 AA.  
AC P55868;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE Putative secreted protein XAG precursor.  
GN XAG.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Cement gland;  
RX MEDLINE=97003224; PubMed=8950563;  
RA Sive H., Bradley L.;  
RT "A sticky problem: the Xenopus cement gland as a paradigm for  
RT anteroposterior patterning";  
RL Dev. Dyn. 205:265-280(1996).  
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).  
CC -!- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVEL IN CEMENT GLAND.  
CC -!- SIMILARITY: HIGH, TO XENOPUS NP77.  
CC  
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CC  
CC EMBL; U76752; AAB1819.1; -  
KW Signal.  
FT SIGNAL  
FT CHAIN 1 18 POTENTIAL.  
FT CHAIN 19 183 PUTATIVE SECRETED PROTEIN XAG.  
SQ SEQUENCE 183 AA; 20475 MW; 95E12B06FCB8DCE8 CRC64;  
Query Match 42.1%; Score 448; DB 1; Length 183;  
Best Local Similarity 49.4%; Pred. No. 9.3e-35;  
Matches 88; Conservative 29; Mismatches 51; Indels 10; Gaps 3;  
QY 39 AFLLLVALSYLTARDTTVKP---GAKTKDKSRPKLP-----QTLSRGWGDLITWQTY 89  
Db SLVCLVLVLCALGEALVKPKKQAGTTQTKDQEPAPIKTKGLTKDGRWGSIEWVQTY 65  
QY 90 EEALYKSTSNKPLMIHHLEDCPSHQALKKVFQENKEIQKLA-EQFVLLNLIYVETDGH 148  
Db EEGLAKARENKPLNVIHLEDCPSYIALKAFVADRWAKLAQEDFIMLNLVHPVADEN 125  
QY 149 LSPDQYVPRIMFVDPDSLTVTVRADITGRYSNRLIYAYEPADTALLDNMKKALKLKTTEL 206  
Db QSPDGHYVPRVIFIDPSLTVTVRADITGRYSNRLIYAYEPADTALLDNMKKALKLKTTEL 183

## ALIGNMENTS

34	74.5	7.0	381	1	PRLP_BOVIN
35	74.5	7.0	905	1	NTC3_MOUSE
36	74.5	7.0	2319	1	NTC3_RAT
37	74.5	7.0	2321	1	NTC3_HUMAN
38	74.5	7.0	5171	1	BPEA_HUMAN
39	74	7.0	260	1	TATD_SCOLI
40	74	7.0	986	1	GM13_RAT
41	74	7.0	1034	1	POL_HV2CA
42	73.5	6.9	233	1	YEG7_YEAST
43	73.5	6.9	695	1	TKT_FICST
44	73.5	6.9	971	1	CSEI_PAGMA
45	73	6.9	316	1	COMA_YERPE

Q9gk8 bos taurus  
Q9qxy1 mus musculus  
Q9rl72 rattus norv  
Q9um47 homo sapien  
Q94833 homo sapien  
P27859 escherichia  
Q62839 rattus norv  
P24107 human immun  
P39983 saccharomyc  
P34736 pichia stip  
Q9pu3 pagrus majo  
Q8zan6 yersinia pe

```
RESULT 2
NP77_XENLA STANDARD; PRT; 185 AA.
ID NP77_XENLA STANDARD; PRT; 185 AA.
AC P5869;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Putative secreted protein NP77 precursor.
GN NP77.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
SEQUENCE FROM N.A.
TI TISSUE=Cement gland;
RA Aberger F., Schueren C., Lepperdinger G., Richter K., Grunz H.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVEL IN CEMENT GLAND
CC (POTENTIAL).
CC -1- SIMILARITY: HIGH, TO XENOPUS XAG.
CC -----
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CC -----
CC EMBL; U82110; AAB49974.1; -.
KW Signal.
DR SIGNAL
FT CHAIN
SQ SEQUENCE 185 AA; 20442 MW; AE3807C926044509 CRC64;

Query Match 41.2%; Score 437.5; DB 1; Length 185;
Best Local Similarity 53.5%; Pred. No. 9.1e-34;
Matches 84; Conservative 26; Mismatches 46; Indels 1; Gaps 1;

QY 51 ARDTTVKPGAKDVKDSRPKLPQTLRSRGDGLWTQTYEALYKSTNSKPLMIHLLD 110
DB 29 AADDTNGAKSEPAVKTGLKLTLDRGWGEDIEWAQTYEGLAKARENKPLMVIHLE 88
QY 111 ECPHSQALKVFAENKEIKLIA-EQFVLLNLVYETTDKHLSPDQYVPRIMFVDPSTLTVR 169
DB 89 DCFYSIALKKAFAVADKWAQKLAQEDFIMNLVHPVADENQSPDGHVYPKGFIDPSLTVR 148
QY 170 ADITGRVSNRLYAVEPADTALLDNNKALKLKTTEL 206
DB 149 SDLKGRYGNKLYAYDADDIPELITNMKAKSFLKTTEL 185

RESULT 3
TL19 MOUSE
ID TL19 MOUSE STANDARD; PRT; 170 AA.
AC Q9CQU0;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Thiorodoxin-like protein p19 precursor (Endoplasmic reticulum protein
DE ERp19).
GN TL19.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
TI TISSUE=Embryo, and Kidney;
RA STRAIN=C57BL/6J;
RC
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Medline=21085660; Pubmed=11217851;  
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
Arakawa T., Harai A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,  
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
Sakai K., Okido T., Furuno M., Anon H., Baldarelli R., Barh G.,  
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
Lyons P., Marchionni L., Maehima J., Mazzarelli J., Mombaerts P.,  
Nardone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
Havashizaki Y.;  
"Functional annotation of a full-length mouse cDNA collection.";  
Nature 409:685-690(2001).  
[2]  
SEQUENCE FROM N.A.  
TI TISSUE=Mammary gland;  
MEDLINE=22388257; Pubmed=12477932;  
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Srausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
Bosak S.A., McEwan P.J., Kerneran K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalley D.E.,  
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
"Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[3]  
SUBCELLULAR LOCATION.  
RA Knoblach B., Keller B.O., Groenendyk J., Aldred S., Zheng J.,  
Lemire B.D., Li L., Michalak M.;  
"ERp19 and ERp46, new endoplasmic reticulum luminal proteins of the  
thiorodoxin family.";  
Submitted (MAR-2003) to the SWISS-PROT data bank.  
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
CC -1- SIMILARITY: Contains 1 thiorodoxin domain.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; AK003481; BAB22811.1; -.  
DR EMBL; AK002862; BAB22413.1; -.  
DR EMBL; BC006857; AAH06857.1; -.  
DR MGI; 1913323; 0610040B21Rik.  
DR InterPro; IPR000886; ER target.  
DR InterPro; IPR006662; Thiorod.  
DR InterPro; IPR006663; Thiorodox\_dom2.  
DR PROSITE; PS00014; ER\_TARGET; 1.  
DR PROSITE; PS00194; THIOREDOXIN; 1.  
KW Endoplasmic reticulum, Redox-active center; Signal.

FT SIGNAL 1 24 POTENTIAL.  
 FT CHAIN 25 170 THIOREDOXIN-LIKE PROTEIN P19.  
 FT DISULFID 64 67 REDOX-ACTIVE (POTENTIAL).  
 FT SITE 167 170 PREVENT SECRETION FROM ER (POTENTIAL).  
 FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 170 AA; 19048 MW; 5B91FC9BE12C5E44 CRC64;

Query Match 21.1%; Score 224.5; DB 1; Length 170;  
 Best Local Similarity 34.9%; Pred. No. 6.4e-14;  
 Matches 58; Conservative 25; Mismatches 58; Indels 25; Gaps 4;

QY 39 AFLIALVALSYLTARDTTVKPGAKTKDSRPLQTLRGWGDQLIWTQTYEALYKSKT 98  
 DB 14 SFLLLITSS-----DGR-----TGLGKGFGDHIHW-RTLEDGKKEAAA 50  
 QY 99 SNKPLMIITHLDECPHSQALKKVFANKEIQKLAEOQVLLNL--VYETDKHLSPDGQV 156  
 DB 51 SGLPLMVLIIHSCWGCACALKPKFAESTEISELSHNFVNVLDEDEEPRDEDFSPDGGYI 110  
 QY 157 PRIMVDPVSLTVRADITGRYSNRLYAYEPADPTALLDNMKKALKLL 202  
 DB 111 PRILFDPSGKVRPIINESGNPSYKVFYVSAEQVVGKKEAQL 156

## RESULT 4

ID TL19 HUMAN STANDARD; PRT; 172 AA.  
 AC Q95881; Q96H50;  
 DT 15-SEP-2003 (Rel. 42, Created)  
 DT 15-SEP-2003 (Rel. 42, Last sequence update)  
 DE Thioredoxin-like protein p19 precursor (Endoplasmic reticulum protein ERP19).  
 GN TLP19.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Mei G., Yu W., Gibbs R.A.;  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Liu F., Rong Y., Zeng L., Qi X., Han Z.;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE=Colon, Kidney, and Ovary;  
 RC MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshitoki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).  
 CC -1- SIMILARITY: Contains 1 thioredoxin domain.

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CC EMBL; AF131758; AAD20035.1; -  
 DR EMBL; AF543416; AAN34781.1; -  
 DR EMBL; BC001493; AAH01493.1; -  
 DR EMBL; BC008953; AAH08953.1; -  
 DR EMBL; BC008913; AAH08913.1; -  
 DR InterPro; IPR006662; Thiredox.  
 DR InterPro; IPR006663; Thiredox dom2.  
 DR PROSITE; PS00194; Thiredoxin\_1.  
 KW Endoplasmic reticulum; Redox-active center; Signal.  
 FT SIGNAL 1 26 POTENTIAL.  
 FT CHAIN 27 172 THIOREDOXIN-LIKE PROTEIN P19.  
 FT DISULFID 66 69 REDOX-ACTIVE (POTENTIAL).  
 FT SITE 169 172 PREVENT SECRETION FROM ER (POTENTIAL).  
 FT CONFLICT 102 102 D -> H (IN REF. 3; AAH08913).  
 SQ SEQUENCE 172 AA; 19206 MW; 3092E9515A7C4094 CRC64;

Query Match 20.9%; Score 222; DB 1; Length 172;  
 Best Local Similarity 34.2%; Pred. No. 1.1e-13;  
 Matches 54; Conservative 26; Mismatches 56; Indels 22; Gaps 3;

QY 66 DSRPKLPOT-----LSRGWGDLIWTQTYEALYKSKTSNPKLMI 106  
 DB 2 ETRPRLGATLLGFSFLLLVISDSHGNGLGKFGDHIHW-RTLEDGKKEAASGLPLMVI 60  
 QY 107 HLDCEPHSQALKKVFANKEIQKLAEOQVLLNL--VYETDKHLSPDGQVPRIMFVDP 164  
 DB 61 IHKSWGCGACKALKPKFAESTEISELSHNFVNVLDEEPEKDEDFSPDGGYIPRILFLDP 120  
 QY 165 SLTVRADITGRYSNRLYAYEPADPTALLDNMKKALKLL 202  
 DB 121 SGKVHPEIINENGNSPYKVFYVSAEQVVGKKEAQL 158

## RESULT 5

YM51 YEAST STANDARD; PRT; 458 AA.  
 ID YM51 YEAST  
 AC P42933;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Hypothetical 52.2 kDa protein in SGS1-MRPL24 intergenic region.  
 GN YMR191W OR YMR646.03.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S288C / AB972;  
 RX PubMed=9169872;  
 RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,  
 RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,  
 RA Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.,  
 RA Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;  
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XIII.";  
 RL Nature 387:90-93 (1997).  
 RN [2]  
 RP SEQUENCE OF 1-249 FROM N.A.  
 RC STRAIN=W303;  
 RX MEDLINE=95059068; PubMed=7969174;  
 RA Gangloff S., McDonald J.P., Bendixen C., Arthur L., Rothstein R.;  
 RT "The yeast type I topoisomerase Top3 interacts with Sgs1, a DNA helicase homolog: a potential eukaryotic reverse gyrase.";

```
RL Mol. Cell. Biol. 14:8391-8398(1994).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z47815; CAA87812.1; -
DR EMBL; U23341; AAB60288.1; -
DR PIR; S50919; S50919.
DR SGD; S0004803; YMR191W.
KW Hypothetical protein.
FT CONFLICT 128 128 N -> Y (IN REF. 2).
FT CONFLICT 132 135 FVTW -> LALG (IN REF. 2).
SQ SEQUENCE 458 AA; 52183 MW; C31107D7B28DAE33 CRC64;

Query Match      8.2%; Score 87.5; DB 1; Length 458;
Best Local Similarity 20.1%; Pred. No. 1.4; Indels 109; Gaps 13;
Matches 55; Conservative 35; Mismatches 74;

QY 15 PSRLTQG-----RWKRSVAMEKIPVSAPFLILVALS----- 47
DB 82 PTRNMAVGNNWSWMLRMSRVHLRQITKSLDRTLISLSHGNSFHOYNNRIFVTWKSLE 141
QY 48 -----YTLARDTTVPKAKKDTK-----DSRPKLQTLNRG-----W-----GD 81
DB 142 ASTAFRASGLTWSPLTRRGIRARDFPRPVNVNPKFASFPVPKGPAGRLFTNNMTTSK 201
QY 82 QLIWTQTYEALYK---SKTSNKLPMI-----IHHLDECPSHQ----- 116
DB 202 RLLGQRAYSTSSIKFTQEAANNMTISURCFNSLGGNLQCHNSCKAYONASNVTSKOD 261
QY 117 -----ALKKV-----PAENKEIQKLAEPVFLNLVYETTDKHLSPGQYV----- 156
DB 262 HVQPVALKLSQKDINFIRNLELPKMK--TQNEVDVETSAYMYKPGSVIETISEFNV 319
QY 157 -----PRIMVDPSLTVRADITGRYSNRLYAYE 184
DB 320 NGTFSAPLSLDRPSLL--ADLDEMIRN--YKYE 348

RESULT 6
MISA_CHICK
ID MYSA_CHICK STANDARD; PRT; 1829 AA.
AC Q02440;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myosin Va (Myosin 5A) (Dilute myosin heavy chain, non-muscle) (Myosin
DE heavy chain P190) (Myosin-V).
GN MYO5A.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93012002; PubMed=1383040;
RA Sanders G., Lichte B., Meyer H.E., Kilmann M.W.;
RT "cDNA encoding the chicken ortholog of the mouse dilute gene product.
RT Sequence comparison reveals a myosin I subfamily with conserved C-
RT terminal domains."
RL FEBS Lett. 311:295-298 (1992).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1154-1163.
RC TISSUE=Brain;
RX MEDLINE=93107155; PubMed=1469047;
RA Espreafico E.M., Cheney R.E., Matteoli M., Nascimeto A.A.,
```

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RA de Camilli P.V., Larson R.E., Mooseker M.S.;
RT "Primary structure and cellular localization of chicken brain
RT myosin-V (p190), an unconventional myosin with calmodulin light
RT chains.";
RL J. Cell Biol. 119:1541-1557(1992).
CC -!- FUNCTION: PROCESSIVE ACTIN-BASED MOTOR THAT CAN MOVE IN LARGE
CC STEPS APPROXIMATING THE 36-NM PSEUDO-REPEAT OF THE ACTIN FILAMENT.
CC MAY BE INVOLVED IN MELANOSOME TRANSPORT, OR ALTERNATIVELY, IT MAY
CC BE REQUIRED FOR SOME POLARIZATION PROCESS INVOLVED IN DENDRITE
CC FORMATION (BY SIMILARITY).
CC -!- SUBUNIT: MAY BE A HOMODIMER, WHICH ASSOCIATES WITH MULTIPLE
CC CALMODULIN OR MYOSIN LIGHT CHAINS.
CC -!- SUBCELLULAR LOCATION: GOLGI-DERIVED CYTOPLASMIC MEMBRANES
CC (POTENTIAL).
CC -!- TISSUE SPECIFICITY: NEURONAL AND NONNEURONAL CELLS OF THE BRAIN.
CC -!- SIMILARITY: Contains 1 myosin-like globular head domain.
CC -!- SIMILARITY: Contains 1 dilute domain.
CC -!- SIMILARITY: Contains 6 IQ domains.
CC -----
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CC -----
DR EMBL; X67251; CAA47673.1; -
DR EMBL; Z11718; CAA77782.1; -
DR PIR; S19188; S19188.
DR HSSP; P10587; 1BR2.
DR InterPro; IPR002710; DIL.
DR InterPro; IPR000048; IQ_region.
DR InterPro; IPR001609; myosin_head.
DR Pfam; PF01843; DIL; 1.
DR Pfam; PF00612; IQ; 6.
DR Pfam; PF00063; myosin_head; 1.
DR PRINTS; PR00193; MYOSINHEAVY.
DR ProDom; PD003376; DIL; 1.
DR ProDom; PD000355; myosin_head; 1.
DR SMART; SM00015; IQ; 6.
DR SMART; SM00242; MYSC; 1.
DR PROSITE; PS50096; IQ; 6.
KW Myosin; Repeat; ATP-binding; Calmodulin-binding; Actin-binding;
KW Coiled coil; Phosphorylation. MYOSIN HEAD-LIKE.
FT DOMAIN 1 766
FT DOMAIN 767 789 IQ 1.
FT DOMAIN 790 814 IQ 2.
FT DOMAIN 815 837 IQ 3.
FT DOMAIN 838 862 IQ 4.
FT DOMAIN 863 887 IQ 5.
FT DOMAIN 888 915 IQ 6.
FT DOMAIN 916 1239 COILED COIL (POTENTIAL).
FT DOMAIN 1315 1419 COILED COIL (POTENTIAL).
FT DOMAIN 1661 1766 DILUTE.
FT NP_BIND 163 170 ATP (BY SIMILARITY).
FT DOMAIN 644 666 ACTIN-BINDING (POTENTIAL).
FT MOD_RES 1734 1734 PHOSPHORYLATION (POTENTIAL).
FT CONFLICT 1142 1142 E -> EQ (IN REF. 2).
SQ SEQUENCE 1829 AA; 212381 MW; 0538B278DFC09F6E CRC64;

Query Match      8.0%; Score 85.5; DB 1; Length 1829;
Best Local Similarity 28.1%; Pred. No. 13;
Matches 27; Conservative 21; Mismatches 41; Indels 7; Gaps 3;

QY 63 DTKDSRPKLPQTLRSRGWQDLWTQTYEALY-KSKTSNKLPMIHHLDCPH--SOALK 119
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB DILLDECKPKGSDDTWAQKLYNHLNKLKALFKPKRLSKAFIKHFAADKVEQCEGLE 566
QY 120 K-----VFAENKEIQKLAEPVFLNLVYETTDKHLSP 151
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 567 KKKDTVYEEQIKVLKSKSKFKLLPELFQDEKAISP 602
```

## RESULT 7

ID RFX1 YEAST STANDARD; PRT; 811 AA.  
AC P48743;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE RFX-like DNA-binding protein RFX1.  
GN RFX1 OR CRT1 OR YLR176C OR L9470.18.  
OS Saccharomyces cerevisiae (Baker's Yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=S288c / AB972;  
RX MEDLINE=97313267; PubMed=9169871;  
RA Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansoerge W.,  
RA Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A.,  
RA Entian K.-D., Floeth M., Goffeau A., Hebling U., Heumann K.,  
RA Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P.,  
RA Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D.,  
RA Mueller-Auer S., Netwich U., Obermaier B., Piravandi E., Pohl T.M.,  
RA Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,  
RA Scharfe M., Scherrens B., Scholler P., Schwager C., Schwarz S.,  
RA Underwood A.P., Urrastazu L.A., Vandenbol M., Verhasselt P.,  
RA Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,  
RA Wedler H., Zimmermann F.K., Zollner A., Hani J., Hohelsel J.D.;  
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";  
RL Nature 387:87-90(1997).  
CC -!- SIMILARITY: BELONGS TO THE RFX FAMILY.  
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CC  
CC EMBL: U17246; AAB67470.1; -  
CC SGB; S0004166; RFX1.  
CC GO; GO:0005737; C:nucleus; IDA.  
CC GO; GO:0005634; C:nucleus; IDA.  
CC GO; GO:0016566; F:specific transcriptional repressor activity; IDA.  
CC GO; GO:0000122; P:negative regulation of transcription from P. .; IDA.  
CC InterPro; IPR003150; RFX\_DNA\_binding.  
CC Pfam; PF02257; RFX\_DNA\_binding; 1.  
KW DNA-binding.  
SQ SEQUENCE 811 AA; 90583 MW; 116A88B7DDE4FBF0 CRC64;

Query Match 7.9%; Score 84; DB 1; Length 811;  
Best Local Similarity 25.7%; Pred. No. 6.4;  
Matches 47; Conservative 29; Mismatches 67; Indels 40; Gaps 8;  
OY 8 LSGSOP-----HPSRLTQGR-----WVRKSRVAMEKIPVSAFLLVALSYTLAR 52  
DB 129 LIGSGPGSHKSPPTTPQPAQATQRTQATSVYPASISLRNSNSAYPLSPKSEETLNN 188  
OY 53 D--TTVK-----PGAKDKTKSRPKLPQTLSRGWDQLTIWTQTYEALYKSKTSNKP 102  
DB 189 NPPTAAKRTNTFPSPISPTKQKTSQEKRISSIRNTQETIIAKQIAEN--NKSXTIEY 246  
OY 103 LMIHH-----LDECHPSOALKKVFABNKIEIKLAEQVLLNLVYETTTDKHSPDQGY 155  
DB 247 AQIVKHAEIKVLKSMDSQNTSKAALQALQNRERER--QVFALLMLMKNCQSHDS---Y 300  
OY 156 VPR 158  
DB 301 VPR 303

## RESULT 8

ID YD67 SCHPO STANDARD; PRT; 217 AA.  
AC Q10319;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Hypothetical protein C17G8.07 in chromosome I.  
GN SPAC17G8.07.  
OS Schizosaccharomyces pombe (Fission yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
OC Schizosaccharomycetes.  
OX NCBI\_TaxID=4896;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=972; PubMed=11859360;  
RX MEDLINE=21848401; PubMed=11859360;  
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,  
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,  
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitz E.,  
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,  
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,  
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,  
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,  
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaue V., Mottier S.,  
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,  
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;  
RT "The genome sequence of Schizosaccharomyces pombe.";  
RL Nature 415:871-880(2002).  
CC -!- SIMILARITY: TO HUMAN AFG9 AND ENL AND YEAST TRANSCRIPTION  
CC -!- SIMILARITY: STRONG. TO YEAST YNL107W.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: Z69795; CAA93690.1; -  
CC PIR; T37859; T37859.  
CC GenDB SPombe; SPAC17G8.07; -  
CC InterPro; IPR005033; YEATS.  
CC Pfam; PF03366; YEATS; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 217 AA; 24946 MW; A274C2AFB0620D7F CRC64;

Query Match 7.9%; Score 83.5; DB 1; Length 217;  
Best Local Similarity 20.6%; Pred. No. 1.3;  
Matches 42; Conservative 33; Mismatches 80; Indels 49; Gaps 8;  
OY 14 HPSRLTQGR-----RWVRKSRVAMEKIPVSAFLLVALSYTLARDTTVKPGAKDKTKD 66  
DB 39 HTWRFIFVEGVGDGDISKWVRK-----VVFKL-----HDTYNNP---TRTIE 76  
OY 67 SRPKLPQTLSRGWDQLTIWTQTYEALYKSKTSNKPLMI IHHLDCEPHSOALKKVFABNK 126

```
Db 77 SPFP--EVITGGEFDMVRIF-----FAPEAHEKALTFFHLKHLHYGPRMEEMKASGG 130
Qy 127 EIOKLAQFVLLNLVYETTKHLSPP-----DQGVPRIMFVDPSTLVTRADITGRYSNRLYA 182
Db 131 LVESVQVEEVFNEPFYTKLLSQNPIGDGH-----GLAVESEPHDPFSQOQLEQ 180
Qy 183 YEPADTALLDNNMKKALKLKTTEL 206
Db 181 DEADKLDFAIQEVKTIEMTKQQV 204

RESULT 9
HSL1 SCHPO
ID HSL1 SCHPO STANDARD; PRT; 507 AA.
AC P50582; O94678;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cell cycle protein kinase hsk1 [EC 2.7.1.1-].
GN HSK1 OR SPBC776.12C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RC STRAIN=JY2;
RX MEDLINE=95347336; PubMed=7621824;
RA Masai H., Miyake T., Arai K.-I.;
RT "hsk1", a Schizosaccharomycetes pombe gene related to Saccharomycetes
RT cerevisiae CDC7, is required for chromosomal replication.;
RL EMBL J. 14:3094-3104(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Scouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford J., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weijtjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffart F., Cadeu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Carrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Uesery D., Bartell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomycetes pombe.";
RL Nature 415:871-880(2002).
CC -1- FUNCTION: REQUIRED FOR CHROMOSOMAL REPLICATION.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=P50582-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=P50582-2; Sequence=VSP_004863;
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CDC7
CC SUBFAMILY.
```

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EMBL; D50493; BAA09087.1; -;  
DR EMBL; AL035263; CAA22885.1; -;  
DR EMBL; AL035263; CAB38417.1; -;  
DR PIR; S56143; S56143.  
DR PIR; T40683; T40683.  
DR GeneDB\_Spombe; SPBC776.12C; -;  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR002290; Ser\_thr\_kinase.  
DR Pfam; PF00069; pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 2.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
KW Cell cycle; Cell division; Serine/threonine-protein kinase;  
KW Transferase; ATP-binding; Alternative splicing.  
FT DOMAIN 68 433 PROTEIN\_KINASE.  
FT NP\_BIND 74 82 ATP (BY SIMILARITY).  
FT BINDING 129 129 ATP (BY SIMILARITY).  
FT ACT\_SITE 216 216 BY SIMILARITY.  
FT VARSPPLIC 92 119 Missing (in isoform Short).  
FT SQ SEQUENCE 507 AA; 58407 MW; 04970E58218441EE CRC64;  
Query Match 7.8%; Score 83; DB 1; Length 507;  
Best Local Similarity 22.4%; Pred. No. 4.3;  
Matches 28; Conservative 24; Mismatches 55; Indels 18; Gaps 5;  
Qy 83 LIWTQYEEALYKSTNKP----LMIHLDSPHSQALKVFAENKIQKLAEOFVLL 138  
Db 380 ILWASCGSASIKYKLRHPSQERCLDFLEKCLDCKKRISAE----EALDHDFLYL 435  
Qy 139 -NLVYETTKHLSPPDQGVPRIMFVDPSTLVTRADITGRYSNRLYAY---EPADTALLDN 194  
Db 436 DNLAYEKDDDTAFDNS-----FGTSPFKDLDLTAHLHILDFKEQEBETDEPTSLSK 489  
Qy 195 MKKAL 199  
Db 490 RKRSI 494  
RESULT 10  
OCRL\_HUMAN  
ID OCRL\_HUMAN STANDARD; PRT; 901 AA.  
AC Q01968; O60800; Q15684; Q15774; Q9JUG5; Q9UMA5;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Inositol polyphosphate 5-phosphatase OCRL-1 (EC 3.1.3.36) (Lowe's  
DE oculocerebrorenal syndrome protein).  
GN OCRL OR OCRL1 OR INPP5F.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM B).  
RC TISSUE=Kidney;  
RX MEDLINE=92334430; PubMed=1321346;  
RA Attree O., Olivos I.M., Okabe I., Bailey L.C., Nelson D.L.,  
RA Lewis R.A., McInnes R.R., Nussbaum R.L.;  
RT "The Lowe's oculocerebrorenal syndrome gene encodes a protein highly  
RL homologous to inositol polyphosphate-5-phosphatase.";  
RN Nature 358:239-242(1992). [2]

```

FT VARIANT 357 357 /FTID=VAR_010169.
FT FT G -> E (IN LOWE SYNDROME).
FT FT /FTID=VAR_010170.
FT VARIANT 367 367 MISSING (IN LOWE SYNDROME).
FT FT /FTID=VAR_010171.
FT VARIANT 372 372 V -> G (IN LOWE SYNDROME).
FT FT /FTID=VAR_010172.
FT VARIANT 375 375 H -> Y (IN LOWE SYNDROME).
FT FT /FTID=VAR_010173.
FT VARIANT 421 421 G -> E (IN LOWE SYNDROME).
FT FT /FTID=VAR_010174.
FT VARIANT 424 424 N -> D (IN LOWE SYNDROME).
FT FT /FTID=VAR_010175.
FT VARIANT 451 451 D -> G (IN LOWE SYNDROME).
FT FT /FTID=VAR_010176.
FT VARIANT 463 463 F -> S (IN LOWE SYNDROME).
FT FT /FTID=VAR_010177.
FT VARIANT 498 498 C -> Y (IN LOWE SYNDROME).
FT FT /FTID=VAR_010178.
FT VARIANT 500 500 R -> G (IN LOWE SYNDROME).
FT FT /FTID=VAR_010179.
FT VARIANT 500 500 R -> Q (IN LOWE SYNDROME).
FT FT /FTID=VAR_010180.
FT VARIANT 508 508 V -> D (IN LOWE SYNDROME).
FT FT /FTID=VAR_010181.
FT VARIANT 513 513 Y -> C (IN LOWE SYNDROME).
FT FT /FTID=VAR_010182.
FT VARIANT 522 522 S -> R (IN LOWE SYNDROME).
FT FT /FTID=VAR_010183.
FT VARIANT 524 524 H -> Q (IN LOWE SYNDROME).
FT FT /FTID=VAR_010184.
FT VARIANT 524 524 H -> R (IN LOWE SYNDROME).

Query Match 7.7%; Score 81.5; DB 1; Length 901;
Best Local Similarity 23.7%; Pred. No. 13;
Matches 45; Conservative 32; Mismatches 46; Indels 67; Gaps 13;

QY 55 TVKPGAKDKDSRPK--LPQTLGRGQDQILMTQVEAL-YKS---KTS-NKPLMII 106
Db 476 TYKYDSKTRDWSGKCRVP-----AMCDRLWRGTWNQNLNYSHEMLKTSDRKPYVAL 530

QY 107 HHL-----DECPHSQALKKVFPAENKEIQKLAE-----QFVLLNLVYETTDK-- 147
Db 531 FHIGVKVDE---RRYRKVFEDSVRIMDRMENDFLPSLSLSRREFVFNKVPQLQKKG 586

QY 148 -HLSPDGQ-----YVPRM-----FVDPSLTVRADITGRYSNRLVAYE 184
Db 587 FQISNNGQVCHFSFIPKLANDSQYCKPWLRAEPPEGYLEPNETV--DIS-----LDVYV 638

QY 185 PADTALLLDN 194
Db 639 SKDSVTILNS 648

RESULT 11
TOP2_PLAFK
ID TOP2_PLAFK STANDARD; PRT; 1398 AA.
AC P41001;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE DNA topoisomerase II (EC 5.99.1.3).
GN TOP2.
OS Plasmodium falciparum (isolate K1 / Thailand).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OC NCBI_TaxID=5839;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94316496; PubMed=8041616;
RA Cheesman S., McAleese S., Goman M., Johnson D., Horrocks P.,
RA Ridley R.G., Kilbey B.J.;
RT "The gene encoding topoisomerase II from Plasmodium falciparum.";
RL Nucleic Acids Res. 22:2547-2551(1994).

```

-I- FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY TRANSIENT  
 BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE II  
 MAKES DOUBLE-STRAND BREAKS.  
 -I- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining  
 of double-stranded DNA.  
 -I- SUBUNIT: Homodimer (By similarity).  
 -I- SUBCELLULAR LOCATION: Nuclear.  
 -I- MISCELLANEOUS: EUKARYOTIC TOPOISOMERASE I AND II CAN RELAX BOTH  
 NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC ENZYMES  
 RELAX ONLY NEGATIVE SUPERCOILS.  
 -I- SIMILARITY: Belongs to the type II topoisomerase family.

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EMBL; X79345; ; NOT\_ANNOTATED\_CDS.  
 HSP; P06786; IEGW.  
 InterPro; IPR003594; ATPbind ATPase.  
 InterPro; IPR003957; CBFA NFYB Topis.  
 InterPro; IPR001241; DNA\_topoisoiI.  
 InterPro; IPR002205; DNA\_topoisoiV.  
 Pfam; PF00204; DNA\_gyras2B; 1.  
 Pfam; PF00521; DNA\_topoisoiV; 1.  
 Pfam; PF02518; HATPase c; 1.  
 PRINTS; PR00615; CCAATSUBUNTA.  
 PRINTS; PR00418; TPI2FAMILY.  
 ProDom; PD000742; DNA\_topoisoiV; 1.  
 SMART; SM00387; HATPase c; 1.  
 SMART; SM00433; TOP2c; 1.  
 SMART; SM00434; TOP4c; 1.  
 DR PROSITE; PS00177; TOPOISOMERASE II; 1.  
 DR ISOMERASE; Topoisomerase; DNA-binding; ATP-binding; Nuclear protein.  
 FT NP\_BIND 144 149  
 FT ACT\_SITE 830 830  
 FT DOMAIN 271 281  
 FT DOMAIN 308 316  
 FT DOMAIN 1089 1093  
 FT DOMAIN 1227 1234  
 FT DOMAIN 1227 1234  
 SQ SEQUENCE 1398 AA; 161029 MW; 6AAD7BEE88FE5BE9 CRC64;

Query Match 7.7%; Score 81.5; DB 1; Length 1398;  
 Best Local Similarity 21.9%; Pred. No. 22;  
 Matches 30; Conservative 25; Mismatches 47; Indels 35; Gaps 5;

QY 85 WTQTYEALYKSTSNKPLMIIHLDCEPHSQALKKVFPAENKEIQKLAEO-----FVLLN 139  
 Db 956 WTQYKEFLLELLTDEKHQILDYINNSHEDICFTIKMDPAKLOKAEESGLEKVKLKS 1015

QY 140 LVYETTDKHLSPDGQVYPRIMFVDPSLTVRADITGRYS-----NRLVAYEPADT 188  
 Db 1016 TLTTT-----NMTLFDPNLKLQ-----RYSTELDLKFCYQRLKAYENR-K 1056

QY 189 ALLDDNMKALKLKTE 205  
 Db 1057 SYLISKLEKRIISNK 1073

RESULT 12  
 YTH6\_RHOER  
 ID YTH6\_RHOER STANDARD; PRT; 339 AA.  
 AC P43484;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical 37.5 kDa protein in thcr 5'region (ORF6).  
 OS Rhodococcus erythropolis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Nocardiaceae; Rhodococcus.

counseling.";

Hum. Mutat. 16:157-165 (2000).

[13]

VARIANTS LS PRO-337 AND GLY-372.

MEDLINE=20232168; PubMed=10767176;

Roschinger W., Munteau A.G., Rudolph G., Roscher A.A.,  
Kammerer S.;

"Carrier assessment in families with Lowe oculocerebrorenal syndrome: novel mutations in the OCRL1 gene and correlation of direct DNA diagnosis with ocular examination.";

Mol. Genet. Metab. 69:213-222 (2000);

-1- FUNCTION: Converts phosphatidylinositol 4,5-bisphosphate to phosphatidylinositol 4-phosphate. Also converts inositol 1,4,5-trisphosphate to inositol 1,4-bisphosphate and inositol 1,3,4,5-tetrakisphosphate to inositol 1,3,4-trisphosphate. May function in lysosomal membrane trafficking by regulating the specific pool of phosphatidylinositol 4,5-bisphosphate that is associated with lysosomes.

-1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-bisphosphate + H(2O) = 1-phosphatidyl-1D-myo-inositol 4,5-bisphosphate.

-1- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

Name=A;

Isoid=Q01968-1; Sequence=Displayed;

Name=B;

Isoid=Q01968-2; Sequence=VSP\_002681;

-1- TISSUE SPECIFICITY: BRAIN, SKELETAL MUSCLE, HEART, KIDNEY, LUNG, PLACENTA, AND FIBROBLASTS.

-1- DISEASE: DEFECTS IN OCRL ARE THE CAUSE OF LOWE'S OCULOCEREBRORENAL SYNDROME, A DISEASE CHARACTERIZED BY HYDROPHALMIA, CATARACT, MENTAL RETARDATION, VITAMIN D-RESISTANT RICKETS, AMINOACIDURIA, AND REDUCED AMMONIA PRODUCTION BY THE KIDNEY.

-1- SIMILARITY: BELONGS TO THE INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE TYPE II FAMILY.

-1- SIMILARITY: Contains 1 Rho-GAP domain.

-1- DATABASE: NAME=Lowe Syndrome mutation database;  
WWW="http://research.nhgri.nih.gov/lowe/";

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EMBL; M88162; AAA59964.1; ALT\_INIT.

EMBL; U57627; AAB03839.2; -

EMBL; AL022162; CAA18150.1; -

EMBL; AL022162; CAA18151.1; -

EMBL; Z73496; CAA97842.1; -

EMBL; S62085; AAB26926.1; -

PIR; S29069; S29069.

Genew; HGNC:8108; OCRL.

MIM; 303000; -

GO; GO:0005795; C:Golgi stack; TAS.

GO; GO:0005798; C:Golgi vesicle; TAS.

GO; GO:0004439; F:Phosphatidylinositol-bisphosphatase activity; TAS.

GO; GO:0006629; P:lipid metabolism; TAS.

InterPro; IPR005135; Exo\_endo\_phos.

InterPro; IPR000300; IPPC.

InterPro; IPR000198; RhoGAP.

Pfam; PF03372; Exo\_endo\_phos; 1.

Pfam; PF00620; RhoGAP; 1.

SMART; SM00128; IPCC; 1.

SMART; SM00324; RhoGAP; 1.

PROSITE; PS50238; RHO GAP; 1.

Hydrolase; Alternative splicing; Disease mutation.

DOMAIN 721 901

DOMAIN 707 914

-----

VARIANT 337 337

Missing (in isoform B).  
R -> P (IN LOWE SYNDROME).



OX NCBI\_TaxID=1833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=NI86/21;  
RX MEDLINE=96082876; PubMed=7583123;  
RA Tamura T., Nagy I., Lupas A., Lottspeich F., Cejka Z., Schoofs G.,  
RA Tanaka K., de Mot R., Baumeister W.;  
RT "The first characterization of a eubacterial proteasome: the 20S  
RT complex of Rhodococcus";  
RL Curr. Biol. 5:766-774(1995).  
RN [2]  
RP SEQUENCE OF 1-333 FROM N.A.  
RC STRAIN=NI86/21;  
RX MEDLINE=95138028; PubMed=7836301;  
RA Nagy I., Schoofs G., Compennolle F., Proost P., Vanderleyden J.,  
RA de Mot R.;  
RT "Degradation of the thiocarbamate herbicide EPTC (S-ethyl  
RT dipropylcarbamothioate) and biosafening by Rhodococcus sp. strain  
RT NI86/21 involve an inducible cytochrome P-450 system and aldehyde  
RT dehydrogenase";  
RL J. Bacteriol. 177:676-687(1995).  
CC -!- SIMILARITY: STRONG, TO M.TUBERCULOSIS RV2097C AND M.LEPRAE  
CC MLCB2533-24.  
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CC  
CC EMBL; U26421; AAC45738.1; -  
DR EMBL; U17130; AAC45747.1; -  
DR InterPro: IPR004347; DUF245.  
DR Pfam: PF01336; DUF245; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 339 AA; 37462 MW; 23CB953F88739599; CRC64;  
Query Match 7.5%; Score 80; DB 1; Length 339;  
Best Local Similarity 29.5%; Pred. No. 4.9; Mismatches 36; Indels 18; Gaps 5;  
Matches 31; Conservative 20;  
M101 KPLMIHDECPHQALKKVFAENKEIQKLAQFVLNLYVETDQKHLSPDQGVVPRIM 160  
M122 RPVTAVHHISHDPTLRA-TVALADGRLTGLAQRIYLDV- ---DKFMSAEGNDPRV- 175  
M161 FVDSPLTVRADITGRYSNRLYAYE--PADTALLLDNMKALKLK 203  
M176 -----ADLLEKWMVLDLLERDPMECAHLLDWPAP-LRLLE 210  
RESULT 13  
YNSL YEAST  
ID YMSL YEAST STANDARD; PRT; 843 AA.  
AC Q05050;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Hypothetical 93.3 kDa protein in TAP42-CYK2 intergenic region.  
GN YMR031C OR YMR9973.04C.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=S288c / AB972;  
RX PubMed=9169872;  
RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,  
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,  
RA Jageis K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.,  
RA Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;  
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome  
RT XIII";  
RL Nature 387:90-93(1997).  
CC -!- SIMILARITY: TO YEAST YKL050C.  
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CC  
CC EMBL; Z49213; CRA89146.1; -  
DR PIR; S53947; S53947.  
DR SGD; S0004633; YMR031C.  
KW Hypothetical protein.  
SQ SEQUENCE 843 AA; 93345 MW; 0068D65A229B941D CRC64;  
Query Match 7.5%; Score 80; DB 1; Length 843;  
Best Local Similarity 21.3%; Pred. No. 16; Mismatches 29; Indels 54; Gaps 7;  
Matches 38; Conservative 29;  
M20 TQGRWKRVRVAMKIPVSAFLIIVL-----LSYTLARDTTVKCAKKDTKDS 67  
M453 TANRHQTEKTSQEKIKAS-FDALVARDTKVABRETTLEDTSKEIEFKQMQLKDE 511  
M68 RPKLPQTLSCRGDQLTWTQYEEALYKSTSNKPLMIHHLDECPHQALKKVFAE--- 124  
M512 KARLDQDLLE-----WGKCEQDITEARKEQBELLPKPYH-DDLANAEAEHKLVEERD 563  
M125 --NKEIQKLARQFV-----LNL--VYETTDKHLSPD 152  
M564 EINAEISLQDAIVDHKKEISGYGNDLDAQNRNIREDDKLELQGTRESLESHLND 621  
RESULT 14  
ERA\_HELPJ STANDARD; PRT; 301 AA.  
AC Q9ZLW0;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE GTP-binding protein era homolog.  
GN ERA OR JHP0466.  
OS Helicobacter pylori J99 (Campylobacter pylori J99).  
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
OC Helicobacteraceae; Helicobacter.  
OX NCBI\_TaxID=85963;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99120557; PubMed=9923682;  
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,  
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,  
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,  
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,  
RA Trust T.J.;  
RT "Genomic sequence comparison of two unrelated isolates of the human  
RT gastric pathogen Helicobacter pylori";  
RL Nature 397:176-180(1999).  
CC -!- FUNCTION: BINDS BOTH GDP AND GTP, HAS AN INTRINSIC GTPASE ACTIVITY  
CC AND IS ESSENTIAL FOR CELL GROWTH (BY SIMILARITY).  
CC -!- SIMILARITY: Belongs to the era/trme family of GTP-binding  
CC proteins. Era subfamily.  
CC -!- SIMILARITY: Contains 1 KH type-2 domain.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC

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CC EMBL; AE001480; AAD06035.1; -
DR PIR; G71929; G71929.
DR HSP; P06616; IEGA.
DR HAMAP; MF 00367; -; 1.
DR InterPro; IPR005662; Era.
DR InterPro; IPR004087; KH dom.
DR InterPro; IPR004044; KH_TYPE 2.
DR InterPro; IPR005225; Small_GTP.
DR Pfam; PF00013; KH; 1.
DR TIGRFAMs; TIGR00436; era; 1.
DR TIGRFAMs; TIGR00231; small GTP; 1.
DR PROSITE; PS0823; KH TYPE 2; 1.
KW GTP-binding; RNA-binding; Complete proteome.
FT NP_BIND 12 19 GTP (POTENTIAL).
FT NP_BIND 64 68 GTP (POTENTIAL).
FT NP_BIND 122 125 GTP (POTENTIAL).
FT DOMAIN 204 280 KH TYPE-2.
SQ SEQUENCE 301 AA; 34485 MW; F668C7730892EDBF CRC64;

Query Match 7.58; Score 79.5; DB 1; Length 301;
Best Local Similarity 27.8%; Pred. No. 4.7;
Matches 25; Conservative 13; Mismatches 33; Indels 19; Gaps 4;

QY 89 YEALYKSKTSNKP-LMIHHLDECPHSQALKVFAENKEIQKLAEOFLV-----137
Db 106 YEBFL---SICQPHILAKSIDTATHKQVLKL----QBYKYSSQFLVPLSAKKSQ 158
QY 138 -LNLVYETTDKHLSPDQGYVPRIMFVPSL 166
Db 159 NLNALLECISKHLSPLSAWLFKDLMSDEKM 188

RESULT 15
TFBI_SCHPO STANDARD; PRT; 477 AA.
ID Q13745;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Putative RNA polymerase II transcription factor TFIIF subunit 1.
GN SPAC16E8.11C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brookes K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
RA Waltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Gaffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
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RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RL "The genome sequence of Schizosaccharomyces pombe.";
CC -!- FUNCTION: Component of the core-TFIIF basal transcription factor
CC (potential).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Contains 2 BSD domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z98529; CAB11039.1; -.
DR PIR; T37791; T37791.
DR GeneDB SPombe; SPAC16E8.11c; -.
DR InterPro; IPR005607; BSD.
DR Pfam; PF03909; BSD; 2.
DR PROSITE; PS0858; BSD; 2.
KW Hypothetical protein; Transcription regulation; Nuclear protein;
KW Repeat.
FT DOMAIN 60 113 BSD 1.
FT DOMAIN 134 185 BSD 2.
SQ SEQUENCE 477 AA; 54558 MW; E21CCF7EC370C34C CRC64;

Query Match 7.4%; Score 79; DB 1; Length 477;
Best Local Similarity 26.3%; Pred. No. 9.5;
Matches 36; Conservative 21; Mismatches 42; Indels 38; Gaps 8;

QY 87 QTYEALYKSKTSNKP-----LMIHHLDEC-----PHS--OALK-----KYPHEN 125
Db 85 QTFKEAVMKHLSNEQFWSTRLHLRAHAVERSQQRGPNVLSITKPTVDNMQKSLTG 144
QY 126 KEIQKLAEOFLNLVYETTDKHLSP--DGOVYPRIMFVPSLTVRADITGRYSNRLYAY 183
Db 145 QQIHDWFQHPPLRKVY---DKHVPPLAGEFWSRFLSKLCKKLKRGD-----RITPM 194
QY 184 EPADTALLLDNMKKALK 200
Db 195 DPSPD-----DINDKYLK 206
```

Search completed: November 26, 2003, 15:55:04  
Job time : 20 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 26, 2003, 15:52:23 ; Search time 35 Seconds  
(without alignments)  
1518.824 Million cell updates/sec

Title: US-09-674-266A-181  
Perfect score: 1063  
Sequence: 1 RLSCAGTLGSGPHPSRLT.....DTALLDNKKALKLKTTEL 206

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_23.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	899	84.6	175	4	O95994
2	828	77.9	175	11	O88312
3	555	52.2	165	11	Q8R3W7
4	555	52.2	166	4	Q8TD06
5	550	51.7	165	11	Q8BW95
6	548	51.6	159	13	Q90Y05
7	447	42.1	185	13	O42251
8	227	21.4	172	4	Q96H50
9	224.5	21.1	170	11	Q9CQU0
10	222	20.9	172	4	O95881
11	199	18.7	186	5	Q9NA78
12	165	15.5	257	5	Q9NS57
13	119	11.2	150	17	O27777
14	113.5	10.7	357	16	Q8EXX9
15	89	8.4	950	11	Q924S5
16	88.5	8.3	737	2	Q9AF04

17	87.5	8.2	824	16	Q8FI25
18	87	8.2	348	16	Q926X3
19	85	8.0	1620	5	Q8IIV3
20	84.5	7.9	378	16	Q8XU3
21	84.5	7.9	1151	16	Q929J2
22	84	7.9	435	5	Q9BJK8
23	84	7.9	463	5	O18141
24	83.5	7.9	268	10	Q8L7Y4
25	83.5	7.9	595	10	Q8L5D2
26	83.5	7.9	918	10	Q9CA88
27	83.5	7.9	1011	5	Q9U9P6
28	83.5	7.9	1409	5	Q9V3A7
29	83.5	7.9	1409	5	Q9U6I2
30	83	7.8	786	4	Q9H747
31	83	7.8	976	5	Q9U158
32	82.5	7.8	788	16	O67557
33	82	7.7	242	5	Q8I428
34	81.5	7.7	649	10	Q9C5B1
35	81.5	7.7	926	16	Q8PF46
36	81.5	7.7	1158	3	Q9UTR5
37	81.5	7.7	1472	5	O8ILC8
38	81.5	7.7	1721	5	Q8SSQ0
39	81	7.6	601	5	Q9J598
40	81	7.6	610	5	Q9XVM2
41	80.5	7.6	802	4	Q8TB22
42	80.5	7.6	875	12	Q9QG39
43	80	7.5	154	16	Q9PCE7
44	80	7.5	259	10	Q9M9H0
45	80	7.5	563	5	Q8I0B7

#### ALIGNMENTS

#### RESULT 1

O95994 PRELIMINARY; PRT; 175 AA.  
 ID O95994;  
 AC O95994;  
 DT 01-MAY-1999 (TRENBLrel. 10, Created)  
 DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)  
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)  
 DE Secreted CEMENT gland protein XAG-2 homolog (Anterior GRADIENT 2  
 DE (XENEPUS LAEVIS) homolog) (XAG-2 homolog long protein).  
 GN HAG-2/R OR HAG-2/C OR HPC8.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RC TISSUE=Breast;  
 RX MEDLINE=99009231; PubMed=9790916;  
 RA Thompson D.A., Weigel R.J.;  
 RT "HAG-2, the human homologue of the Xenopus laevis cement gland gene  
 RT XAG-2, is coexpressed with estrogen receptor in breast cancer cell  
 RT lines.";  
 RL Biochem. Biophys. Res. Commun. 251:111-116(1998).  
 RN [2]  
 RC TISSUE=Colon;  
 RX MEDLINE=99009231; PubMed=9790916;  
 RA Zhang J.S., Smith D.I.;  
 RT "Human homolog of XAG is differentially expressed in tumors.";  
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RC TISSUE=Colon;  
 RX MEDLINE=99009231; PubMed=9790916;  
 RA Strausberg R.;  
 RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RC TISSUE=Colon;  
 RX MEDLINE=99009231; PubMed=9790916;  
 RA Zhang J.S., Smith D.I.;  
 RT "Identification of human homolog of XAG-2 over-expressed in tumors.";  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF038451; AAC82614.1; -.

```
DR EMBL; AF007791; AAC77358.1; -
DR EMBL; AF088867; AAF22484.1; -
DR EMBL; BC015503; AAH15503.1; -
DR EMBL; AF115926; AAH54870.1; -
DR Genew; HGNC:328; AGR2.
SQ SEQUENCE 175 AA; 19979 MW; F271B1BD377BEE11 CRC64;

Query Match      84.6%; Score 899; DB 4; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-80;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 MEKIPVSFALLLVSYTLARDTTVKPGAKDTPKSRPKLPQTLSRGWGDLIWTQYEE 91
DB 1 MEKIPVSFALLLVSYTLARDTTVKPGAKDTPKSRPKLPQTLSRGWGDLIWTQYEE 60

QY 92 ALYKSTSNKPLMIHHLDECPHSQALKKVFPAENKEIQKLAEQFVLLNLVYETTDKHLSP 151
DB 61 ALYKSTSNKPLMIHHLDECPHSQALKKVFPAENKEIQKLAEQFVLLNLVYETTDKHLSP 120

QY 152 DGQYVPRIMFVDPSSLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLKTTEL 206
DB 121 DGQYVPRIMFVDPSSLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLKTTEL 175

RESULT 2
O88312 PRELIMINARY; PRT; 175 AA.
AC O88312;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GGB-4 protein (Anterior GRADIENT 2) (XENOPUS LAEVIS) (XENOPUS LAEVIS).
DE LAEVIS).
GN AGR2 OR GGB-4 OR MAG-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP STRAIN=SWISS WEBSTER;
RC STRAIN=SWISS WEBSTER;
RX MEDLINE=99009231; PubMed=9790916;
RA Thompson D.A., Weigel R.J.;
RT "hKX-2, the human homologue of the Xenopus laevis cement gland gene XAG-2, is coexpressed with estrogen receptor in breast cancer cell lines."
RL Biochem. Biophys. Res. Commun. 251:111-116(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikola I., Pesole G., Quackenbush J.,
RA Schirml L.M., Stauber P., Suzuki R., Tonita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Bono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
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RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtauki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AB016592; BAA32044.1; -
DR EMBL; AF044262; AAC72705.1; -
DR EMBL; AK007677; BAB25181.1; -
DR EMBL; BC013334; AAH13334.1; -
DR MGD; MGI:1344405; Agr2.
SQ SEQUENCE 175 AA; 19920 MW; ACC3CFE429B668CA CRC64;

Query Match      77.9%; Score 828; DB 11; Length 175;
Best Local Similarity 91.4%; Pred. No. 1.8e-73;
Matches 160; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 32 MEKIPVSFALLLVSYTLARDTTVKPGAKDTPKSRPKLPQTLSRGWGDLIWTQYEE 91
DB 1 MEKIPVSFALLLVSYTLAKDTTVKSGAKDPKSRPKLPQTLSRGWGDLIWTQYEE 60

QY 92 ALYKSTSNKPLMIHHLDECPHSQALKKVFPAENKEIQKLAEQFVLLNLVYETTDKHLSP 151
DB 61 ALYKSTSNRPLMVIHHLDECPHSQALKKVFPAENKEIQKLAEQFVLLNLVYETTDKHLSP 120

QY 152 DGQYVPRIMFVDPSSLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLKTTEL 206
DB 121 DGQYVPRIMFVDPSSLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLKTTEL 175

RESULT 3
O883W7 PRELIMINARY; PRT; 165 AA.
AC O883W7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to anterior gradient protein 3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC023499; AAH23499.1; -
SQ SEQUENCE 165 AA; 19081 MW; 39F8C7DCB36E122C CRC64;

Query Match      52.2%; Score 555; DB 11; Length 165;
Best Local Similarity 64.1%; Pred. No. 1.2e-46;
Matches 107; Conservative 28; Mismatches 20; Indels 12; Gaps 4;

QY 41 LLLVALSYTLARDTTVKPGAKDTPKSRPKLPQTLSRGWGDLIWTQYEEALYKSTSN 100
DB 10 LLLITVSSNLA--IAIK-----KEKRP--PQTLSRGWGDDITWVQTYEEGLFHAKSN 58

QY 101 KPLMIITHLDECPHSQALKKVFPAENKEIQKLAEQFVLLNLVYETTDKHLSPDQYVPR 159
DB 59 KPLMIVTHLDECOYCOALKEKFAKNEIQEAMQNDIFMLNLMHETTDKNLSPDQYVPR 118

QY 160 MFVDPSSLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLKTTEL 206
DB 119 MFVDPSSLTVRADITGRYSNRLYAYEPQDLPMLVDNMKKALRLIQSEL 165

RESULT 4
O8TD06 PRELIMINARY; PRT; 166 AA.
ID O8TD06
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Q8TD06;
01-JUN-2002 (TRENBLrel. 21, Created)
01-JUN-2002 (TRENBLrel. 21, Last sequence update)
01-JUN-2002 (TRENBLrel. 21, Last annotation update)
Anterior gradient protein 3.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
(1)
SEQUENCE FROM N.A.
Adam P.J., Boyd R., Fletcher G.C., Tyson K., Terrett J.;
"Proteomic Characterization of Breast Cancer Cell Membranes.";
Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
EMBL; AY069977; AAL55402.1; -.
SEQUENCE 166 AA; 19171 MW; BLA4804B47705D65 CRC64;

Query Match      52.2%; Score 555; DB 4; Length 166;
Best Local Similarity 64.7%; Pred. No. 1.2e-46;
Matches 108; Conservative 28; Mismatches 19; Indels 12; Gaps 4;

QY 41 LLLVALSYTLARDTTVPKAKKDTKDSRPKLPQTLRSRGWGDQIWTQTYEALYKSTSN 100
Db 11 LLLTVSSNLA--IAIK-----REKRP--PQTLRSRGWGDITWQTYEGLFQAQSK 59

QY 101 KPLMIHHLDECPHQALKKVFAENKEIOKLAEOFLVLLNVYETTKHLSPDGQVVPRI 159
Db 60 KPLMVIHLEDCQYQALKKVFAENKEIQEAMQNFIMLNMHETTKNLSPDGQVVPRI 119

QY 160 MFVDPSTLRADITGRYSNRLYAYEPADTALLDNMKKALKLKTTEL 206
Db 120 MFVDPSTLRADITGRYSNRLYAYEPADTALLDNMKKALKLRIQSEL 166

RESULT 5
Q8BW95 PRELIMINARY; PRT; 165 AA.
AC Q8BW95;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE weakly similar to secreted CEMENT gland protein XAG-2 homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
(1)
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AK053177; BAC35297.1; -.
SEQUENCE 165 AA; 19139 MW; 243BC7D9A27A173D CRC64;

Query Match      51.7%; Score 550; DB 11; Length 165;
Best Local Similarity 63.5%; Pred. No. 3.8e-46;
Matches 106; Conservative 28; Mismatches 21; Indels 12; Gaps 4;

QY 41 LLLVALSYTLARDTTVPKAKKDTKDSRPKLPQTLRSRGWGDQIWTQTYEALYKSTSN 100
Db 10 LLLTVSSNLA--IAIK-----REKRP--PQTLRSRGWGDITWQTYEGLFHAKSN 58

QY 101 KPLMIHHLDECPHQALKKVFAENKEIOKLAEOFLVLLNVYETTKHLSPDGQVVPRI 159
Db 59 KPLMVIHLEDCQYQALKKVFAENKEIQEAMQNFIMLNMHETTKNLSPDGQVVPRI 118

QY 160 MFVDPSTLRADITGRYSNRLYAYEPADTALLDNMKKALKLKTTEL 206
Db 119 MFVDPSTLRADITGRYSNRLYAYEPADTALLDNMKKALKLRIQSEL 165

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RESULT 6
Q80Y05 PRELIMINARY; PRT; 159 AA.
ID Q80Y05;
AC Q80Y05;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Cement gland-specific protein CGS
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=83355;
(1)
SEQUENCE FROM N.A.
Alexandrova E.M., Novoselov V.V., Zarskiy A.G.;
"Three novel genes expressed in the anterior part of the Xenopus
laevis embryo.";
Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
EMBL; AF314056; AAL26844.1; -.
SEQUENCE 159 AA; 18275 MW; 738D6228483888EB CRC64;

Query Match      51.6%; Score 548; DB 13; Length 159;
Best Local Similarity 60.0%; Pred. No. 5.7e-46;
Matches 105; Conservative 26; Mismatches 28; Indels 16; Gaps 1;

QY 32 MEKIPVSFLLLVSYTLARDTTVPKAKKDTKDSRPKLPQTLRSRGWGDQIWTQTYEE 91
Db 1 METVLKSLFFLLVATSFYLAKE-----RKQTLRSRGWGDNLWVQTYEE 44

QY 92 ALYKSKTSNKPIMIIHHLDECPHQALKKVFAENKEIOKLAEOFLVLLNVYETTKHLS 151
Db 45 GLFKAENKPELLLNHRNDCPHSQALKAFAEHQGIQKLAEEFLLNVVYDPTDKNLQ 104

QY 152 DGQYVPRIMFVDPSTLRADITGRYSNRLYAYEPADTALLDNMKKALKLKTTEL 206
Db 105 DGQYVPRIMFVDPSTLRADITGRYSNRLYAYEPADTALLDNMKKALKLKTTEL 159

RESULT 7
Q42251 PRELIMINARY; PRT; 185 AA.
ID Q42251;
AC Q42251;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE Cement gland-specific.
GN XAG-2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=83355;
(1)
SEQUENCE FROM N.A.
TISSUE=Head;
MEDLINE=89324051; PubMed=2752418;
Sive H.L., Hattori K., Weintraub H.;
"Progressive determination during formation of the anteroposterior
axis in Xenopus laevis.";
Cell 58:171-180 (1989).
(2)
SEQUENCE FROM N.A.
TISSUE=Head;
RA Sive H.L., Mainstock D.H., Kennedy B.S.;
Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
EMBL; AF025474; AAB91968.1; -.
SEQUENCE 185 AA; 20498 MW; D6CDE02DEC3B857B CRC64;

Query Match      42.1%; Score 447; DB 13; Length 185;
Best Local Similarity 50.6%; Pred. No. 6.2e-36;

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Matches 89; Conservative 26; Mismatches 49; Indels 12; Gaps 2;
QY 43 LVLSYTLARDTTTKP-----GAKOTKDSRPKLPQTLSRGWGDLIWTQYEE 91
Db 10 LVLLCSVLGSAARLKKRQAGATNGAASEPAPVTKGLKTLDRWGSDIEWAQYEE 69
QY 92 ALYKSTSNKPLMIHHLDECPHSQALKVFAENKETQKLA-EQVLLNLVYETDKHLS 150
Db 70 GLAKARENPLMVIHLEDCPSYIALKKAFAVDKMAQKLAQEDFIMNLVHPVADENQS 129
QY 151 PDGQYVPRIMFVPSLTVRADITGRYSNRLYAYEPADTALLDNMKALKLLKTEL 206
Db 130 PDGHVPRVIFIDPSLTVRSDLKGRYGNKLYAYDADDIPELITNMKKAFLKTEL 185

RESULT 8
QY6H50 PRELIMINARY; PRT; 172 AA.
AC Q96H50;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Ovary;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC008913; AA08913.1; -
DR InterPro; IPR006662; ThioRedox_dom2.
DR PROSITE; PS00194; THIOREDOXIN; 1.
KW Hypothetical protein.
SQ SEQUENCE 172 AA; 19228 MW; 5C9DDA6D5A7C4BDF CRC64;

Query Match 21.4%; Score 227; DB 4; Length 172;
Best Local Similarity 34.8%; Pred. No. 2.5e-14;
Matches 55; Conservative 25; Mismatches 56; Indels 22; Gaps 3;

QY 66 DSRPKLPQT-----LSRGWGDLIWTQYEEALYKSTNKPMLII 106
Db 2 ETRPLGATCLLGFSEFLLVSSDCHNGLKGFGDHIHW-RTLEDGKKEAASGLPLMVI 60
QY 107 HHLDECPHSQALKVFAENKETQKLAEQVLLNLVYETTDKH--LSPDGQYVPRIMFVDP 164
Db 61 IHKSWCCKALKPKFAESTEISELSHNFVWVNLDEEPEPKHEDFSPDGGYIPRILFLDP 120
QY 165 SLTVRADITGRYSNRLYAYEPADTALLDNMKALKLL 202
Db 121 SGKVHPPIINENGPNPSYKYFVSAEQVVGQMKEAQERL 158

RESULT 9
QY9CQ00 PRELIMINARY; PRT; 170 AA.
AC Q9CQ00;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 0610040B2IRIK protein (RIKEN CDNA 0610040B21 gene).
GN 0610040B2IRIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; Tissue=Embryo, and Kidney;
RX MEDLINE=21085660; PubMed=11217851;
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Ozawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Kazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bareh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald C., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayaishizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; AK003481; BAB22811.1; -
DR ENBL; AK002862; BAB22413.1; -
DR ENBL; BC006857; AAH06857.1; -
DR MGD; MGI:1913323; 0610040B2IRIK.
DR InterPro; IPR000886; ER target.
DR InterPro; IPR006662; ThioRed.
DR PROSITE; PS00014; ER TARGET; 1-
DR PROSITE; PS00194; THIOREDOXIN; 1.
SQ SEQUENCE 170 AA; 19048 MW; 5B91FC9BE12C5E44 CRC64;

Query Match 21.1%; Score 224.5; DB 11; Length 170;
Best Local Similarity 34.9%; Pred. No. 4.4e-14;
Matches 58; Conservative 25; Mismatches 58; Indels 25; Gaps 4;

QY 39 AFLLIVALSYTLARDTTTVKPAKOTKDSRPKLPQTLSRGWGDLIWTQYEEALYKSKT 98
Db 14 SFLLITSS-----DGR-----TGLGKGFGDHIHW-RTLEDGKKEAAA 50
QY 99 SNKPLMIHHLDECPHSQALKVFAENKETQKLAEQVLLNL--VYETTDKHLSPDGQYV 156
Db 51 SGLPLMVIHKSCKGCKALKPKFAESTEISELSHNFVWVNLDEEPEPRDEDFSPDGGYI 110
QY 157 PRIMFVPSLTVRADITGRYSNRLYAYEPADTALLDNMKALKLL 202
Db 111 PRILFLDPGKVRPEINSGNPSYKYFVSAEQVVGQMKEAQERL 156

RESULT 10
QY5881 PRELIMINARY; PRT; 172 AA.
AC Q95881;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein (Thioredoxin-like protein p19).
GN TLP19.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9620727; PubMed=8619474;
RA Andersson B., Wentland M.A., Ricafrente J.Y., Liu W., Gibbs R.A.;
RT "A 'double adaptor' method for improved shotgun library
construction.";
RL Anal. Biochem. 236:107-113(1996).
RN [2]
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RP SEQUENCE FROM N.A.
RX MEDLINE=97264341; PubMed=9110174;
RA Yu W., Andersson B., Worley K.C., Muzny D.M., Ding Y., Liu W.,
RT Ricafrente J.Y., Wentland M.A., Lennon G., Gibbs R.A.;
RL "Large-scale concatenation cDNA sequencing.";
RN Genome Res. 7:353-358(1997).
RP SEQUENCE FROM N.A.
RA Mei G., Yu W., Gibbs R.A.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon, and kidney;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Liu F., Rong Y., Zeng L., Qi X., Han Z.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF131758; AAD20035.1; -
DR EMBL; BC001493; AAH01493.1; -
DR EMBL; BC008953; AAH08953.1; -
DR EMBL; AF543416; AAN34781.1; -
DR InterPro; IPR006662; ThioRedox_dom2.
DR InterPro; IPR006663; ThioRedox_dom2.
DR PROSITE; PS00194; THIOREDOXIN; 1.
KW Hypothetical protein.
SQ SEQUENCE 172 AA; 19206 MW; 3092E9515A7C4094 CRC64;

Query Match 20.9%; Score 222; DB 4; Length 172;
Best Local Similarity 34.2%; Pred. No. 7.8e-14;
Matches 54; Conservative 26; Mismatches 56; Indels 22; Gaps 3;

QY 66 DSRPKLPQ-----LSRGMGDLIWTQYEEALYKSKTSNKLMLII 106
DB 2 ETRPLGATCLLGFLLIIVSDGNGLGKFGDHIHW-RTLEDGKKAASGLPLMI 60

QY 107 HHLDECPHSQALKKVFPAENKEIQKLAEQFVLNL--VYETTDKHLSPDQGYVPRIMFVDP 164
DB 61 IHKSCGACKALKPKFAESTSELSHNFVWVNLDEDEEPKDEDFSPDGYIPRILFLDP 120

QY 165 SLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKL 202
DB 121 SGKVHPEIINENGPNPSYKYFYVSAEQVQGMKEAQERL 158

RESULT 11
Q9NA78 PRELIMINARY; PRT; 186 AA.
AC Q9NA78;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Y57A10A.23 protein.
GN Y57A10A.23.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Smye R.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wohldmann P., Nhan M., Chissoe S., Hawkins J.;
RT "The sequence of C. elegans cosmid F49H12."
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006642; AAF39830.1; -
DR WormPep; F49H12.5; CE20835.
DR InterPro; IPR000886; ER target.
DR InterPro; IPR006663; ThioRedox_dom2.
DR PROSITE; PS00014; ER_TARGET; 1.
KW Hypothetical protein.
SQ SEQUENCE 257 AA; 30205 MW; BF7FBA62D04DBED6 CRC64;

Query Match 15.5%; Score 165; DB 5; Length 257;
Best Local Similarity 30.7%; Pred. No. 5.5e-08;
Matches 51; Conservative 35; Mismatches 58; Indels 22; Gaps 8;

QY 41 LLLVALSVTLARDTTVPKCAKKTQDSRPKLPQTLSRGMGDLIWTQYEEALYKSKTSN 100
DB 3 LLLLSL---LAVAVLAKKESKEIKD-----LSHGVPSEAIEWE-FDKAIGIAKDLN 50

QY 101 KPLMIHHLDECPHSQALKK---KVFPAENKEIQKLAEQFVLNLV--YETTDKHLSPDQGY 155
DB 51 KPIPFILHKTWCGACKSLKRELKSPKTDLEILILSRKFMVNVNDEDEPDKYSPDGY 110

QY 156 VPRIMFVDPSTVRADITGRYSNRLYAYE-PADTALLLDNMKKAL 199
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Db 315 VDNPIYLSMDGAALTGAESHEL--QDVLEETNIIKRLYKALSLLKKE 359

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Job time : 37 secs

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